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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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US-08-283-17-16-8
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R-914-999-7 R-914-999-7 Rent No. 6346406 ENERAL INFORMATION: APPLICANT: Ryazano APPLICANT: Hait, W APPLICANT: Pavur, TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES	tcacta tcacta ctgtgg 	ctgcca ctgcca	Match Local Simi	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		344.66 344.66 344.22 344.22 332.23 332.23 332.23 332.23 332.23 332.23
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 7:
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1901 GTATATTAGGTACCAATCTCTACAGTGGCTCCTATGATAAAACTATAAGAGTTTGGAATT 1960
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HYPOTHETICAL: N
ORIGINAL SOURCE:
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LENGTH: 2237 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
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REFERENCE/DOCKET NUMBER: 60
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                                           agtacagggacaggctggtagtgagtggctcatctgacaacactatcagattatgggaca 1438
                                                                                              TGAAAACTTTTCGTTGTAACTACACTCTAAAAGGTCATACTAAATGGGTCACCACTATCT
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Pred. No. 2.3e-16;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
APPLICANT: HUBBARD SEL-10 AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08899578 Patent No. 6087153
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INFORMATION FOR SEQ ID NO:
                 1393 ctggtagtgagtggctcatctgacaacactatcagattatgggacatagaatgtggtgca 1452
                                                                               1078
                                                                                                                                                                               1273 tacattgtttctgcatctggggatagaactataaaggtattggaacacaagtacttgtgaa 1332
     1138
                                                                                                           1333 tttgtaaggaccttaaatggacacaaacgaggcattgcctgtttgcagtacagggacagg 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                   1018 TATATTGTTAGCGGGTCCACTGATAGAACTGTAAAAGTTTGGAGGTACTGTAGATGGTTCA 1077
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                   Local Similarity
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ATACTTGTCACTGGATCACGAGATACCACTCTTCGTGTATGGGACGTAGAATCCGGACGT 1197
                                                                       gatttgataacaagaggatagtcagtggggcctatgatggaaaaattaaagtgtgggatc 1558
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                                                                                                                                                                                                                                             Score 67.2; DB 3; Pred. No. 2.1e-11;
                                                                                                                                                                                                                             Mismatches 158;
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                                                                                                      US-08-283-917-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08283917 Patent No. 5849557
    Query Match
Best Local Similarity
Matches 262; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
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ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME TITLE OF INVENTION: AND GENE THEREOF NUMBER OF SEQUENCES: 31
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                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
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NAME: Oblon, No. 5849557man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ADDRESSEE: NEUSTADT, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                         LOCATION:
                                                                                                                                           NAME/KEY:
                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                 LENGTH:
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2.4%; Score 50.8; DB 2; ilarity 47.3%; Pred. No. 4.4e-06; Conservative 0; Mismatches 277:
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US-08-961-716-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 8, Application US/08961716
Patent No. 5880272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: ADACHI
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                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                             SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME TITLE OF INVENTION: AND GENE THEREOF NUMBER OF SEQUENCES: 31
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                                                                                                                                                                                                                                                                                                    STREET: 1755 S. CITY: Arlington STATE: Virginia
                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              COUNTRY: UZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & ADDRESSEE: NEUSTADT, P.C.
                                                                                       FILING DATE:
                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
FILING DATE:
                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgcacttgcgtttcaataatgg-----catgatggtgacctgctccaaagatcgttcca 1174
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1755 S. Jefferson Davis Highway, Suite 400
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ARAI, HIROYUKI
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  03-AUG-1994
                                                                                                           US/08/961,716
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    Sequence 14,

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Best Local Similarity 47.3%;
Matches 262; Conservative
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                                                                                                                                   1529 cctatgatggaaaa 1542
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Oblon, No. 588 REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                     aaggccatgaggaattggtgcgttgtattcgatttgataacaagaggatagtcagtgggg 1528
                                                                                                                                                                                                                                                                                                                                           ACAGAGAATGGGTACGTATGGTGCGGCCAAATCAAGACGGCACTCTGATAGCCAGCTGTT 1600
                                                                                                     TCTCTGAAGCAACA 1734
                                                                                                                                                                                                                                                                CCAATGACCAGACTGTGCGTGTATGGGTCGTAGCAACAAAGGAATGCAAGGCTGAGCTTC 1660
                                                                                                                                                                                                                                                                                                  catctgacaacactatcagattatgggacatagaatgtggtgcatgtttacgagtgttag 1468
                                                                                                                                                                                                                                                                                                                                                                                  acaaacgaggcattgcctgtttgcagtacaggga-----caggctggtagtgagtggct 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAATGTTTCTTCAGTAGCCATCATGCCCAATGGAGATCATATAGTGTCTGCCTCAAGGG 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   accgagctgctgtcaatgttgtagactttgatgacaagtacattgtttctgcatctgggg 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttgctgtatgggatatggcctccccaactgacattaccctccggagggtgctggtcggac 1234
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Application US/08232463
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ER: 24,618
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US-08-232-463-14
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Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
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886 ttacagtatgatgatcagaaaatagtaagcggccttcgagacaacaacaatcaagatctgg
                                                                                                                                                                                                                                                                                                                                                                                 586 gaacttgtgtgcaaggaatggtaccgagtgacctctgatggcatgctgtggaagaagctt 645
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PRIOR APPLICATION DATA:
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APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G.
                                                                                                                                                                  766 agagcactttatcctaaaattatacaagacattgagacaatagaatctaattggagatgt 825
                                                                                                                                                                                                                                                                                                              646 atcgagagaatggtcaggacagattctctgtggagaggcctggcagaacgaagaggatgg 705
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TOPOLOGY: lin
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                                                                                          ggaagacatagtttacagagaattcactgccgaagtgaaacaagcaaaggagtttactgt 885
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                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 218; Mismatches 168; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             2.3%; Score 50; DB 1; Length 7218; 4.9%; Pred. No. 1.9e-05;
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
FENGTH: 2152 base pairs
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                                                                                                                                                                               Matches
                                                                                                                                                                                                Query Match 2.2%;
Best Local Similarity 52.6%;
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TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
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NAME: Osman, Richard A
REGISTRATION NUMBER: 36,
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MEDIUM TYPE: Floppy disk
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                                                          1325 cttgtgaatttgtaaggaccttaaatggaccacaacgaggcattgcctgtttgcagta-- 1382
                                                                                                         1625 ATTCTAATTATGTTGCTACGGGCTCTGCAGACAGAACTGTGCGGCTCTTGGGACGTCCTGA 1684
                                                                                                                                        1265 atgacaagtacattgtttctgcatctggggatagaactataaaggtatggaacacaagta 1324
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1383 ----cagggacaggctggtagtgagtggctcatctgacaacactatcagattatgggaca 1438
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA
                                   FEATURE:
                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
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TOPOLOGY: li
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4 Embarcadero Center, Suite 3400
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Tanese, Naoko
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                                                                                                                                                                               Conservative
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                                                                                                                                                                                 0; Mismatches 112;
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Query Match 2.2%;
Best Local Similarity 52.6%;
Matches 131; Conservative
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                                                                                                                                                                                                                                                                              TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 17:
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Rel-Base #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/188,582 FILING DATE: 28-JAN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                  FEATURE:
                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 09-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
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                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                              LOCATION:
                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                             NAME:
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                           Osman, Richard A
                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
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                                                                                                                                                                                                                                             2152 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wang, Edith
Weinzierl, Robert O.J.
WEINZIERL TATA-BINDING PROTEIN ASSOCIATED FACTORS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tjian, Robert
Comai, Lucio
                                                                                                                                                                                                                                                                                                                    (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Tanese, Naoko
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                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
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                                                                                                                                                                                                          double
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                                                                                                                                                                                                                                                                                                                                                                                        36,627
     0; Mismatches 112;
                         Score 47.8; DB 1;
Pred. No. 4.3e-05;
                                          Length 2152;
         Indels
         6;
       Gaps
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1265 atgacaagtacattgtttctgcatctggggatagaactataaaggtatggaacacaagta 1324

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US-08-232-463-14
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          Matches
                     Best Local Similarity
                                      Query Match
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                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           APPLIANCE AND ANTER ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
NAME: BENT, STEPHEN A.
NAME: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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APPLICANT:
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                                                                                                                                       TOPOLOGY:
                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                  TELEX:
                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/232,463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Alexandria
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          14;
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     Conservative 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                 (703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DORNER, F
                                                                                                                                  linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Foley & Lardner
                                                                                                                                                                                                                                                                 (703)836-9300
                                                                                                                                                 single
               1.9%; Score 39.8; DB 1; 3.6%; Pred. No. 0.042;
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   Mismatches
     167;
                                 Length 7218;
   Indels
   0;
 Gaps
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1,
                                           TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO: 1:
              SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
                                                                         TELEPHONE: (617) 498-8224
                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                      STREET: b, STREET: Cambridge CITY: Cambridge cTATE: Massachusetts
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Spaulding, Vikki
APPLICANT: Bowman, Michael
TITLE OF INVENTION: SECRETEI
TITLE OF INVENTION: ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                  02140
nucleic acid
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5807703
         433 base pairs
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                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treacy, Mauri
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCoy, John
LaVallie, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Merberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                         Genetics Institute,
                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                         514
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Best Local S
Matches 89
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                             Query Match
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                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617), 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
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APPLICANT:
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TOPOLOGY: linear
MOLECULE TYPE: cDN
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 CAGGACACGTTAATGGGACATGATGATGCTGTTAGTAAGATCTGTTGGCATGACAACAGG
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                 y Match 1.8%;
Local Similarity 51.4%;
                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Cambridge
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                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                433 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 CambridgePark Drive
                                                                                                                                                                                                 : (617) 876-5851
(617) TD NO: 1:
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LaVallie, Edward
                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                               linear
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                            Score 38.6; DB 1; Length 433;
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                 Pred. No.
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                 0.015;
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                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 876-58 INFORMATION FOR SEQ ID NO:
                                                                                                     1396 gtagtgagtggctcatctgacaacactatcagattatgggacatagaatgtggtgcatgt 1455
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                     1456 ttacgagtgttagaaggccatgaggaattggtgcgttgtattcgatttgataacaagagg 1515
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 733 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION UMBER: 32,724
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES TITLE OF INVENTION: ENCODING THEM NUMBER OF SEQUENCES: 8
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167 CAGGACACGTTAATGGGACATGATGCTGTTAGTAAGATCTGTTGGCATGACAACAGG 226
                                                                      107 GTCATAACTTCTTCATGGGATAATAATGTCTATTTTATTCCATAGCATTTGGAAGACGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 CAGGACACGTTAATGGGACATGATGATGCTGTTAGTAAGATCTGTTGGCATGACAACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 CTATATTCTGCATCGTGGGACTCTACAGTGAAGGTGTGGTCTGGTGTTCCTGC
                                                                                                                                                Local Similarity nes 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                    TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
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87 CambridgePark Drive
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Treacy, Maurice
Spaulding, Vikki
                                                                                                                                                                                                                                                                                                                                                                                          (617) 876-5851
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LaVallie, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
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                                                                                                                                              Score 38.6; DB Pred. No. 0.022; 0; Mismatches
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; NAME/KEY: CDS
; LOCATION: (13)..(2766)
US-09-156-425-1
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US-09-156-425-1
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
                                                                             Matches
                                                                                                                Query Match
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Best Local
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LENGTH: 3380
TYPE: DNA
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                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING,
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/156,425B
CURRENT FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 47
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APPLICANT: Cowsert, Lex M.

TITLE OF INVENTION: ANVISENSE MODULATION OF FAN EXPRESSION
FILE REFERENCE: RTS-0009
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                               LENGTH: 18596
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                       750 teceaaetetttttatagageaetttateetaaaattataeaagaeattgagaeaataga 809
                                                                                               Local Similarity
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                                                                                             Score 36.6; DB Pred. No. 0.89;
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                                                                                                            DB 4; Length 18596;
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US-08-751-189-2
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APPLICANT: Robinson,
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                     6473 CGTGAGCGCCGTGGTTGCTGTGGAGGAACACATTGTATCTGTGAGCCGAGATGGGACCTT 6532
                                                                                                                                                                                                                                               STREET: 10. CITY: Thousand Oaks
STATE: California
6533 GAAAGTGTGGGACCATCAGGGTGTGGAGCTGACCAGCATCCCTGC 6577
                                                                                                                                          6413 GGGACTCTGGAACCCAGAGGCAGGCAGCTTGGCCAGTTCTCAGGCCACCAGAGTGC 6472
                                                                                                                                                                           1425 cagattatgggacatagaatgtggtgcatgtttacgagtgttagaaggccatgaggaatt 1484
                                                                                                                                                                                                                 6353 CACTGGCTGTGCGTGGACCAAAGACATCCTGGTCTCCTGCTCGAGTGATGGCTCTGT 6412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Oleski, Nancy A. REGISTRATION NUMBER: 34,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Result No.

Query Score Match Length DB

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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JOURNAL EATURES	LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM ORGANISM AUTHORS	ULT 1950:	443	38 440 310	35 37	26 27 28 30 31	18 19 20 21 22 23 24	22 24 44 44 47 47 47 47 47 47 47 47 47 47 47
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1999; R); CONCORDET JEAN PAUL (FR); INST , MATHIAS (FR); DURAND HERVE (FR); IN FLORENCE (FR); PASTEUR INSTITUT CONSTRUCT	NA linear PAT 07-SEP-2000		ALO495/2 Human DNA ALO49522 Human DNA AJ428938 Xenopus 1 AF391190 Mus muscu	AF391186 Mus muscu AF391181 Mus muscu AL137159 Human DNA AC095034 Homo sapi	ACOUTS44 DIOSOPHIL AE003733 DIOSOPHIL ACO14085 DIOSOPHIL U28730 Caenorhabdi . AL44546 3 Human DNA	AX057148 Sequence U63921 Xenopus lae U63922 Xenopus lae U63922 Xenopus lae BC008552 Mus muscu AF339101 Heteroder AF275253 Caenorhab AL627424 Human DNA	AP000252 Homo sapi AP000134 Homo sapi AP000117 Homo sapi AP000211 Homo sapi AP001711 Homo sapi AF032878 Drosophil AF222923 Drosophil	AX019507 Sequence AX057166 Sequence Y14153 Homo sapien AF129530 Homo sapien AF081887 Mus muscu AF101784 Homo sapi BC003989 Mus muscu AF110396 Mus muscu AF110396 Mus muscu AF09932 Mus muscu AF12979 Mus muscu AF12979 Mus muscu AF13281 Homo sapi AB033279 Homo sapi AB033281 Homo sapi AB033281 Homo sapi AB033281 Homo sapi AB014596 Homo sapi AR0738079 Mus muscu

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GAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAG
                                                                        GAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTC
                                                                                         CCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCT
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TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAG
TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDFAAQAEPPRSPSRTYTY
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LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMKFRDSLMRGLAERRGWGOYLFK
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DQKIVSGLRDNTIKINDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDV
NTGEMLNTLIHHCEAVLHLRRNNGMNVTCSKDRSIAVNDMASSTDJTLRRVLVGHRAA
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/db_xref="GI:10043428"
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/translation="ModeAVLOEKALKFMNSSEREDCNNGEDPRKIIDEKNSLROTY
/TRANSLATION="MODEAVLOEKALKFMNSSEREDCNNGEDPRKIISASYEKEKELCV
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/codon_start=1
/transl_table=11
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1740 1740	gatgacacaatcctcatctgggacttcctaaatgatccagctgcccaagctgaacccccc 	168 168	DŁ Qy
1680 1680	. cattccggaagagtttttcgactacagtttgatgaattccagattgtcagtagttcacat 	16 16	Qy dd
1620 1620	gtggctgctttggacccccgtgctcctgcagggac	156 156	DF OS
1560 1560	tttgataacaagaggatagtcagtggggcctatgatggaaaaattaaagtgtgggatctt 	15 15	D 0
1500 1500	1 gaatgtggtgcatgtttacgagtgttagaaggccatgaggaattggtgcgttgtattcga 	144 144	Оу
1440 1440	tacagggacaggctggtagtgagtggctcatctgacaacactatcagattatgggacata 	136 136	₽ <i>Q</i>
1380 1380	ttgtaaggaccttaaatggacacaaacgaggcattgcctgtttgcag 	132 132	B 8
	1 tttgatgacaagtacattgtttctgcatctggggatagaactataaaggtatggaacaca	126 126	D 20
1260 1260	actgacattaccctccggagggtgctggtcggacaccgagctgctgtcaatgttgtagac	120 120	D 0
1200 1200	1 ggcatgatggtgacctgctccaaagatcgttccattgctgtatgggatatggcctccca 	11 11	B 8
1140 1140	acgttgattcaccattgtgaagcagt 	108	Б 8
1080	1 agagtgatcataacaggatcatcggattccacggtcagagtgtgggatgtaaatacaggt 	102 102	Dt Oy
1020 1020	1 gaatgcaagcgaattotcacaggccatacaggttcagtcctctgtctccagtatgatgag 	96 96	5 d
960	. cagaaaatagtaagcggccttcgagacaacacaaatcaaga 	90	Db Qy
900	1 cagagaattcactgccgaagtgaaacaagcaaaggagtttactgtttacagtatgatgat 	84 84	D 8
840 840	1 aaaattatacaagacattgagacaatagaatctaattggagatgtggaagacatagttta 	78 78	dd VQ
780 780	1 aaaaacaaacctcctgacgggaatgctcctcccaactctttttatagagcactttatcct		<u> </u>

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TGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAAT
           tgtttagcaagcactgctatgaagactgagaattgtgtggccaaaaccaaaaacttgccaat
                                                   aattcacttagacagacatacaacagctgtgccagactctgcttaaaccaagaaacagta
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                                           tttgatgacaagtacattgtttctgcatctggggatagaactataaaggtatggaacaca
                                                                      ACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGAC
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                                                                                                                                             GAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATAAT
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                       Mammalia: EULIGELE.

1 (bases 1 to 2151)

Margottin_F., Bour,S.P., Durand,H., Selig,L., Benichun,...,

Richard,V., Thomas,D., Strebel,K. and Benarous,R.

A novel human WD protein, h-beta TrCp, that interacts with HIV-1

Vpu connects CD4 to the ER degradation pathway through an F-box

Vpu connects CD4 to the TrCp.
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Benarous, R.
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GAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAA
                     gaacatcttatatcccaaatgtgtcattaccaacatgggcacataaactcgtatcttaaa
                                                                                          AAGGAACTGTGTGAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTG
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LSYLDAKSLCAAEDVCKEWYRVTSDGMLWKKLIERMVEYDSLWRGLAERRGWGQLFK
NKPPDGNAPRAGFYRALYPKIIODIETIESNWRGGRHSLQRTHGRSETSKGYVCLYV
NKPPDGNAPRAGFYRALYPKIIODIETIESNBRGGWGTYDERVIITGSSDSTVRVWDV
DOKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDV
NTGEMLNTLIHHCEAVLHLRENNGMYTCSKDRSIAVWDMASPFDITLERVLVGHRAA
VNVVDEDDKYIVSASGDRTIKVMNTSTCEFVRTLNGKRGIACLQYRDRLVVSGSSDN
TIRUDIECGACLRVLEGHEELVRCIIRDNKRIVSGAYDGKIKWWDLVAALDPAAPAG
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/cell_type="T lymphocyte"
/tissue_type="lymphoid"
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/db_xref="taxon:9606"
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AF129530
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 2151)
Cenciarelli,C., Chiaur,D.S., Gand Dagger
                                                                                                     Submitted (19-FEB-1999) Pathology, Ave. MSB 548, New York, NY 10016, 1
                                                                                                                          Chiaur, D.S. and Pa
Direct Submission
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AF129530.1
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                    Identification of a family of Curr. Biol. 9 (20), 1177-1179
                                                                                                                                                                                         and Pagano, M.
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                                                                                                                                                                                                                                                       human
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          /gene="FBW1A"
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                                                                                   1. .2151
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                                .2151
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chromosome 10 F
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F-box protein FbwlA (FBWlA) mRNA,
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                                                                                                                                                                     human
(1999)
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                                                                                                                  NYU Medical Center,
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                                                                       GAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTC
                                                                                                                                                               GAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAG
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VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAG
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KYFEQNSESDOVEFVEHLISOMCHYQHGHINSYLKPMLJCRDFTTALPARGLDHIAENI
LSYLDAKSLCAAELVCKEMYRVTSDGMLMKKLIERMVRCDSLMRGLAERRGWQVLFK
NKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHGRSETSKGVYCLQV
DCKIVSCLRDNTIKINDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVMDV
DCKIVSCLRDNTIKINDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVMDV
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forms an SCF with Skp1 and Cull"
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0		74	Db
1800	gttccccttctcgaacatacacctacatctccagataaataa		Qy
1740	GATGACACAATCCTCGTGTGTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCCCCC	1681	DЬ
1740	atgacacaatcctcatctgggacttcctaaatgatccagctgcccaagctgaaccccc	1681	Qy
1680	CATTCCGGAAGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACAT	1621	Db
1680	attccggaagagtttttcgactacagtttgatgaattccagattgtcagtagttcacat		Qy
1620	GTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAG		Дb
1620	tggctgctttggacccccgtgctcctgcagggacactctgtctacggacccttgtggag	1561	Qy
1560	TTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTT	1501	Db
1560	ttgataacaagaggatagtcagtggggcctatgatggaaaaattaaagtgtgggatctt	1501	Qy
1500	GAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGA	1441	Db
1500	aatgtggtgcatgtttacgagtgttagaaggccatgaggaattggtgcgttgtattcga	4	Qу
1440	TACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATA	1381	Db
1440	acagggacaggctggtagtgagtggctcatctgacaacactatcagattatgggacata	w	Qy
1380	TTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAG		DЬ
1380	gtacttgtgaatttgtaaggaccttaaatggacacaaacgaggcattgcctgtttgca	1321	Оу
1320	TTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACA	N	Db
	tyatyacaaytacattyttctycatctygggatagaactataaaygtatygaacac	1261	Qy
1260	ACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGAC	2	Db
1260	ctgacattaccctccggagggtgctggtcggacaccgagctgctgtcaatgttgtagac	1201	Qy
	GCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCA	1141	Db
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14	GAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATAAT		DЪ
1140	aaatgotaaacacgitgattoaccattgtgaagcagttotgcacttgcgtttcaataa	1081	Qy
80		.02	Db
1080	gagtgatcataacaggatcatcggattccacggtcagagtgtgggatgtaaatacagg		Qy
	GAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCCAGTATGATGAG	961	Db
1020	aatgcaagcgaattctcacaggccatacaggttcagtcctctgtctccagtatgatg	961	Qy
960	CAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACATTG	901	Дb
960	agaaaatagtaagcggccttcgagacaacacaatcaagatctgggataaaaacacatt	901	Qy
900	CAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGAT	841	DЪ
900	agagaattcactgccgaagtgaaacaagcaaggagtttactgtttacagtatgatga	841	Qу
840	AAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTA	781	Db
840	aaattatacaagacattgagacaatagaatctaattggagatgtggaagacatagttt	781	Qy
780	AAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTTATATCCT		дд
	.aaaacaaacctcctgacgggaatgctcctcccaactctttttatagagcactttatcc	721	Qy
720	${\tt AGGACAGATTCTCTGTGGAGAGGGCCTGGCAGAACGAAGGAGGATGGGGACAGTATTTATT$	661	Db

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                                                                                                                                                                                                                                                                                                                                        Submitted (04-AUG-1998) Department of Molecular and Cellular Biology, Medical Institute of Bioregulation, Kyushu University, 3-1-1, Maedashi, Higashi-ku, Fukuoka 812-8582, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2175)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus ubiquitin ligase FWD1 mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ubiquitin ligase Skp1/Cul 1/F-box protein FWD1
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3859-3863 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ubiquitin-dependent degradation of IkappaBalpha is mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hattori, K., Higashi, H., Nakano, H., Okumura, K., Onoe, K.,
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           KYFEOWSESDOVEFVEHLISOMCHYOHGHINSYLKPMLQRDFITALPARGLDHIAENI
LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERWYRTDSLWRGLAERRGWCQYLFK
LKYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERWYRTDSLWRGLAERRGWCQYLFK
KKPPDEBAPPNSFYRALYPKIIQDIETLESNWRCGRHSLQRIHGRSETSKGYVCLQYD
DQKIVSGLRDNTIKIWDKSTLECKRILTGHTGSVLCLQYDDERVIITGSSDSTVRVWDV
NAGEMLNTLIHHCEAVLHAERNHGMMYTCSKDRSIAVWDMASFTDITLERVLYGHRAA
VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLMAALDFRAPAG
                                                                                                                        /product="ubiquitin ligase FWD1"
/protein_id="AAD17755.1"
/protein_id="AAD17755.1"
/db_xref="G1:4336327"
/translation="MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
/translation="MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
NSCARLCINQETYCLTSTAMKTENCVAKAKLANGTSSMIVPKORKLSASYEKEKELCV
                                                                                                                                                                                                                           protein TrcP; F-box
                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAHAEPPRSPSRTYTY
                                                                                                                                                                                                                                            /note="similar to beta-transducin repeat-containing
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                                                                                       CC---GGCTGCCTCAGTGCTGCTATCAGAAGATGTCTT-TATCTTGTGTGAATGATTGGA
                                                                                                                                                     TTTGAGACTCCTGTTGGGACACAGTCGGTCAGCAGCCGGA-CCAGGACGGCCTGCTCGGCA 1991
                                                                                                                                                                                                                                                       -----AACAATCAAACTCCTACCCGGATTCCCGGACGGATGAGCGAGGAGCAGGGC 1932
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                  232 gaaacagtatgtttagcaagcactgctatgaagactgagaattgtgtggccaaaacaaaa
                                                               211 CCAGAGAAGAATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA
                                                                                                                                                  151 TTCCAGAATTCCTCAGAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 210
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                                                                                       Submitted (27-OCT-1998) Immunology, Hebrew University-Hadassah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yaron, A., Hatzubai, A., Davis, M., Lavon, I., Amit, S., M. Andersen, J.S., Mann, M., Mercurio, F. and Ben-Neriah, Y. Identification of the receptor component of the IkappaBalpha-ubiquitin ligase Nature 396 (6711), 590-594 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medical School, Jerusalem, Israel
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1 (bases 1 to 1818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mann, M. and Ben-Neriah, Y.
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TGALTAFONSSEREDCNINGEPPRKIIPEKNSLROTYNSCARLCLNQETYCLASTAMKT
ENCYAKTKLANGTSSMIYPKORKLISASYEKEKELCYKYFEQWASEDQVEFVEHLISQM
CHYQHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRV
TSDGMLWKKLIERMYRTDSLWRGLAERKGWGOYLFKNKPPDGNAPPNGFYRALYPKII
QDIETIESNWRCGRHSLORIHCRSETSKGYYCLQYDDQKIVSGLLRDNTIKIWDKNTLE
CKRILTGHTGSYLCLQYDERYIITGSSDSTYRWDDYNTGEMLMYLIHHCEAVLHLRFN
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WNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEEL
VRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="b-TRCP variant E3RS-IkappaB
/protein_id="AAD08702.1"
/db_xref="G1:4165136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="beta-transducin repeats-containing protein;
receptor component of IkappaBa-ubiquitin ligase; contains
F-box and WD regions"
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gttgtagactttgatgacaagtacattgtttctgcatctggggatagaactataaaggta
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                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, web site:

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl. Series: IRAK Plate: 8 Row: o Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 675
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-FEB-2001) National Institutes of He Gene Collection (MGC), Cancer Genomics Office, Na Institute, 31 Center Drive, Room 11A03, Bethesda,
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BASE COUNT
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VNVVDFDDKYIVSASGDRTIKVMNTSTGEFVRTLNGKKRGIACLQYRDKLVVSGSSDN
TIRLWDIECGACLRYLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLMAALDPRAPAG
TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAHAEPPRSPSRTYTY
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NKPPDENAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYD
DQKIVSGLRDNTIKIWDKSTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDV
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arose spontaneously from a senescent normal mammary
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Winston,J., Elledge,S.J. and Harper,J.W.
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     Mammalia; Eutheria;
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                 Metazoa;
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     Chordata;
Rodentia;
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                Vertebrata; Euteleostomi;
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atatcccaaatgtgtcattaccaacatgggcacataaactcgtatcttaaacctatgttg
                                                                                                TGTGTCAAGTATTTTGAGCAGTGGTCAGAGTCTGATCAAGTGGAATTTGTAGAACACCTT
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                                                                                                                                                                                                   AGCATGATTGTGCCCAAGCAGCGGAAACTCTCAGCAAGCTATGAGAAGGAAAAGGAGCTG
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IkappaBalpha-ubiquitin 11989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (19-OCT-1998) Immunology,
Ein Karem, Jerusalem 91120, Israel
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VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLMAALDPRAPAG
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NSCARLCINGETVCLTSTANKTENCYAKAKLANGTSSMIVPKORKLSASYEKEKELCV 
KYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLORDFITALPARGLDHIAKN 
LSYLDAKSLCAAELVCKEWYRYTSOGMLWKKLIERMYRTDSLWRGLAERRGWGQYLFK 
NKPPDENAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYD 
DQKIVSGLRDNTIKIWDKSTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDV
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/protein_id="AAD08701.1"
/db_xref="G1:4008020"
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DQKIVSGLRDNTIKINDKSTLECKRILTGHTGSVLCLQYGERVITTGSSDSTYRVWDV
NAGEMLNTLIHHCEAVLHLRFNNGMMYTCSKDRSIAVWDMASPTDITLRVLVGHRAA
VNVVDEDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLMAALDPRAPAG
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/note="beta-TrCP; F-box protein; IkB-ubiquitin ligase;
substrate recognition subunit of SCF complex; similar
Homo sapiens beta-TrCP and Drosophila melanogaster Sli
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LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFK
                                                                                                                                                                                                              /product "beta-transducin repeat containing protein"
/protein_id="AAD04181.1"
/db_xref="G1:4140718"
/tanslation="MDDAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
/txanslation="MDDAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
/XSCARLCINQETYCLTSTAMKTENCVAKAKLANGTSSMIVPKQRKLSASYEKEKELCV
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                              gtgacctgctccaaagatcgttccattgctgtatgggatatggcctccccaactgacatt 1209
                                                              ATCACAGGCTCCTCAGACTCCACCGTCAGAGTGTGGGATGTAAATGCAGGTGAGATGCTA
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beta-transducin repeats.
Xenopus laevis (library: S. cerevisiae expression
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1 (bases 1 to 1671)
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/db_xref="taxon:8355"
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phiopidfalparglidhiaenilsyldaksilcsaelvckeyfrytsocmlwkklier
myttdslwfglaerrgwgoylfknkppdgktppnsfyralfyddiftiesnwrcg
RHSLORIHCRSETSKGYVCLOYDDQKIVSGLRONTIKIWDKWTLECKRYLMGHTGSV
CLOYDERVIITGSSDSTYRWDDYNTGEMLNTLIHHCEAVLHLRENNGMWVTCSKDRSI
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GHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVS
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                   Homo sapiens BTRCP2 mRNA for F-box and beta-TRCP2 isoform A, complete cds. AB033279
                                                           WD-repeats
                                                                                  linear
                                                           protein
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Qγ Ър Qy В Qy В QY

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KEYWORDS SOURCE ORGANISM FEATURES REFERENCE REFERENCE JOURNAL MEDLINE TITLE JOURNAL TITLE AUTHORS AUTHORS Direct Submission
Submitted (05-0CT-1999) Masaru Katoh, National Cancer Center, Genetics Division; Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, (E-mail:mkatoh@ncc.go.jp, Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685) Katoh, M Biochem. Biophys. Res. 20160458 Katoh, M.
Molecular cloning Eukaryota; Metazoa;
Mammalia; Eutheria; BTRCP2; F-box and WD-repeats Homo sapiens fetal lung cDNA chromosome 5q35.1 Koike, J., Homo sapiens AB033279.1 GI:7209808 (bases 1 to (sites) Location/Qualifiers Sagara, N., Kirikoshi, H., Takagi, A., Miwa, T., Hirai, M. and 2134) and Chordata; Primates; genomic structure Commun. protein beta-TRCP2
to mRNA. Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. 269 (1), of the betaTRCP2 103-109 (2000 Tokyo 104-0045, Japan isoform 14-MAR-2000 gene

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GTCTGCAATATGATGAGAGAGTAATCATTACTGGCTCTTCAGACTCTACCGTCCGGGTGT

936

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TTGCAGAGGATTCAGTGCCGCTCTGAAAATAGTAAAGGTGTCTACTGTTTACAGTACGAT
                                                    ttacagagaattcactgccgaagtgaaacaagcaaaggagtttactgtttacagtatgat
                                                                                                                                                                                                                                        TTTAAAAACAGACCCACAGATGGC------CCTCCAAATTCATTTTATAGGTCATTATAC
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/db_xref="GI:7209809"
/db_xref="GI:720980
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102. .1628
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102. .1628
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/gene="BTRCP2"
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Pred. No. 4.5e-243;
0; Mismatches 371;
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SOURCE KEYWORDS VERSION ACCESSION DEFINITION AB033280 LOCUS ORGANISM

Вþ Qy В Qy 뫄 δÃ В δÃ B Qγ Дb QΥ Вþ Qy Вb δÃ Вb Qy 맑 QY

2252 bp mRNA linear PRI 1. Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein beta-TRCP2 isoform B, complete cds. BTRCP2; F-box and WD-repeats Homo sapiens fetal lung cDNA Homo sapiens AB033280.1 GI:7209810 AB033280 protein beta-TRCP2 isoform to \mbox{mRNA} . PRI 14-MAR-2000

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
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ivsrkrpsegnvqkekolcikyfdqweesddyefvehlisrwchyghghinsylkpml
qrdeitalpeqgldhiaenilsyldarsicaaeluckempgruisegmlwkkilemwt
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Asatditlrruyggssdntikuddiegaclkylegheelukgirstcefyktlngkrg
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157. .1746
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                                                    CATGATGACACTATTTTGATTTGGGATTTCTTAAATGTGCCTCCCAGTGCCCAGAATGAG 1704
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                                                                                                                                                                                                                                                            Local
        9t9gaacatcttatatcccaaatgtgtcattaccaacatgggcacataaactcgtatctt 477
                                                                       GAAAAAGACTTGTGTATTAAATATTTTGACCAGTGGTCTGAATCAGATCAAGTGGAATTT
                                                                                                         9aaaaggaactgtgtgtcaaatactttgagcagtggtcagagtcagatcaagtggaattt 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (05-OCT-1999) Masaru Katoh, National Cancer Center, Genetics Division; Tsukiji 5-Chome, Chuo-ku, Tokyo 104-0045, Japan (E-mail:mkatohéacc.go.jp, Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685)
                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Katoh, M
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                                                                                                                                                                                                                                                                                                                                                                                    /translation="MEPOSVIEDKTIELMGSVDRSLWLGGANLVESWGALSCLOSMPS
/KCLQISMGTSSVIVSRKRPSECNYQKEKDLCIKYPDQWSESDQVEFVEHLISRMCHY
QHGHINSYLKPMLQRDFITALPEOGLDHIAENILSYLDARSLCAAELVCKEWQRVISE
GMLMKKLIEMWVETDPLMKGLSERRGWDQYLFKNRPYDGPPNSFYRSLYPKIIQDIEF
IESNWRGGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVL
TGHTGSVLCLQYDERVIYTGSSDSTYRWWDVNYGEVLNYTLIHHEAVLHLRRSNGLMV
TCSKDRSIAVMDMASAYDITLRRVLYGGRSDVNYGEVLNYTLIHHEAVLHLRRSNGLMV
TCSKDRSIAVMDMASAYDITLRRVLYGGRSDNTIRLWDIEGGACLRVLEGHEELVRCIR
FDNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLKTLVEHSGRVFRLQFDEFQIISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAA92331.1"
/db_xref="GI:7209813"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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74.8%;
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                                                                                                                                                                                                                                Score 883.4; DB 9;
Pred. No. 4.5e-243;
0; Mismatches 371;
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                                                                                                                                                         CAGTACAGGGATCGCCTGGTTGTTAGTGGATCATCAGATAATACCATTAGGCTCTGGGAT 1426
                                                                                                                                                                                  cagtacagggacaggctggtagtgagtggctcatctgacaacactatcagattatgggac 1437
                                                                                                                                                                                                                                                                  acaagtacttgtgaatttgtaaggaccttaaatggacacaaacgaggcattgcctgtttg 1377
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                                                                                                                                                                                                                                           ACGAGCACCTGTGAATTTGTTCGTACTCTCAATGGGCACAAGCGGGGCATTGCCTGTCTC
                                                                                                                                                                                                                                                                                                                                                gactttgatgacaagtacattgtttctgcatctggggatagaactataaaggtatggaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                ccaactgacattaccctccggagggtgctggtcggacaccgagctgctgtcaatgttgta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aatggcatgatggtgacctgctccaaagatcgttccattgctgtatgggatatggcctcc 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGAAGTTCTTAACACATTGATCCACCACAATGAGGCTGTATTGCACTTACGCTTCAGC 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggtgaaatgctaaacacgttgattcaccattgtgaagcagttctgcacttgcgtttcaat 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGAAAAATTATCAGTGGCCTACGAGATAATTCTATTAAGATATGGGATAAAACCAGC 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gatcagaaaatagtaagcggccttcgagacaacaatcaagatctggggataaaaacaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res.
98403880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Submitted (26 MAY-1998) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishikawa,K., Nagase,T., Suyama,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro DNA Res. 5 (3), 169-176 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens mRNA for KIAA0696 F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens adult male brain cDNA to mRNA, clone_lib:pBluescriptII SK plus clone:HK04053.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
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ORIGIN

y 1258 gactttgatgacaagtacattgtttctgcatctggggatagaactataaagqtatggaac 1317 	Qy
NY 1198 ccaactgacattaccctccggagggtgctggtcggacaccgagctgctgtcaatgttgta 1257	Оу
	Qу
<pre>2y 1078 ggtgaaatgctaaacacgttgattcaccattgtgaagcagttctgcacttgcgtttcaat 1137 </pre>	Db Qy
89	Db Qy
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2y 838 ttacagagaattcactgccgaagtgaaacaagcaaaggagtttactgtttacagtatgat 897 	Db Qy
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Oy 538 gotgagaacattotgtoatacotggatgocaaatcactatgtgctgctgcaacttgtgtgc 597	Qy Db
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41 29	Db Db
Qy 358 gaaaaggaactgtgtgtcaaatactttgagcagtggtcagagtcagatcaagtggaattt 417 	Qy Db
Qy 298 aatggcacttccagtatgattgtgcccaagcaacggaaactctcagcaagctatgaaaag 357	Db Db
Query Match 41.1%; Score 883.4; DB 9; Length 4230; Best Local Similarity 74.8%; Pred. No. 4.9e-243; Matches 1122; Conservative 0; Mismatches 371; Indels 6; Gaps	

DЬ γQ Ър Qy δÃ DЬ 20 DЪ Qy B Qy Ъ Qy Ъ Qy 망 1558 cttgtggctgctttggacccccgtgctcctgcagggacactctgtctacaggacccttgtg 1617 1133 GACTTTGACGACAAGTACATCGTGTCTGCCTCTGGTGACAGGACCATCAAAGTCTGGAGC 1192 1433 TTGCAAGCTGCTCTTGACCCTCGAGCCCCAGCAAGCACATTGTGTTTGCGCACACTTGGTG 1492

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Job time: 14986 sec

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17740.707 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                  Description
                                  Human cell signall Human bone marrow
                                                                                                                                                                 Sequence encoding F -box protein hBe
                                                                                                                                                                                                                                     CDNA encoding a hu
Human beta-TrCP co
                                                                                                   Human bone
                                                                                                                                  Human
                                                                                                                                  ZF11 protein
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DNA encoding a F-b	DNA	3552	20	126	5.8	124.4	45
n polynucleoti	Human	AAK53244	22	413		63	44
immune/haem	Human	AAK77731	22	_	٠	67.	43
_	Human	7	22	16532	7.8	167.8	42
: #7692 L	Probe	7	22	370	9.7	08.	41
#15982 used	Probe	AAI47296	22	370	9.7	208.4	40
#11938	Probe	N	22	370	9.7	80	39
Ħa	Humai	41	22	370	9.7	80	38
n brain expres	Human	AAK15524	22	370	9.7	208.4	37
#12638	Probe	ABA34172	22	370	9.7	8	36
foeta	Human	ABA67080	22	370	9.7	80	35
breast	Human	916	22	370		80	34
#2737 use	Probe	AAI02746	22	479		272	33
#2870 used	Probe	AAI34184	22	479		272	32
#2761 for g	Probe	AAI12828	22	479		272	31
bone m		AAK28263	22	479		272	30
brain expi	Humar	AAK02821	22	479		272	29
#2778 f	Probe	ABA24312	22	479		272	28
foetal	Human	ABA54530	22	479		272	27
n breast cell		ABA44075	22	479		272	26
Drosophila melanog		ABL06080	23	9129	13.4	288	25
TRCP.N/SKP2.C		AAC84601	22	1561		18	24
Differentiation In		AAZ09025	20	647	26.6	72	23
Drosophila melanog		ABL06081	23	2387			22
n polynucleoti		AAI59364	22	4360	41.1	83.	21
g	Human	AAK52260	22	4344	41.1	83.	20
	Human	AAA51228	21	4230	•	83.	19
bo	Human	AA161150	22	2084	•	83	18
ubiquitin l	Mouse	AAA73131	21	1707		44	17
protein FWE	F-box	AAZ93714	21	2175	•	682.	16
polynucleot	Human	AAK51716	22	2207		688.	15
polynucleot	Human	AAK51717	22	2366	78.9	7	14
polynucleot	Human	171	22	2285	•	697.	13
beta-transd	Human	313	21	1707	79.4	17	12
_	Human	AAK52701	22	3003	93.4	•	11
	Human	AAK52700	22	3003	93.4	008.	10

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ALIGNMENTS

AAX86501 standard; cDNA; 2151 BP.

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Beta-transducin repeat containing protein; beta-TrcP; Skplp; proteosome degradation pathway; Vpu protein; beta-catenin; human immune deficiency virus-1; HIV-1; cellular protein; IKappaB; ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's; antiviral; antitumour; cell cycle regulation; protein degradation; and anti-inflammatory; osteo-articular inflammation; acute inflammation;
                                                                                                                                                                                                                                                                                                   cDNA encoding a human beta-transducin repeat containing protein.
                                       05-AUG-1999.
                                                                                                                                                                      Homo
                                                                                                                                                                                               tumour necrosis factor; ss.
                                                                                                                                                                                                                                                                                                                            30-SEP-1999 (first entry)
             29-JAN-1999;
                                                                WO9938969-A1.
                                                                                                                                                                     sapiens.
             99WO-FR00196
                                                                                                                 Location/Qualifiers 70..1779
/*tag= a
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/product= beta-TrcP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human beta-transducin repeat containing CC protein (beta-TrcP). The protein directs proteins to the proteosome CC degradation pathways. The protein is able to interact with the Vpu CC protein of human immune deficiency virus-1 (HIV-1), cellular proteins CC LappaB or beta-catenin (bC) and/or protein snd thus their targeting to cubiquitinylation of phosphorylated proteins and thus their targeting to CC proteosomes for degradation. Depending on whether the process is CC inhibited or promoted, the result may be delayed breakdown of CD4 (in CC cases of HIV-1) infection); increased activity of IKB (and thus reduced CC activity of NFkappaB) and increased degradation of mutant bc in tumour CC cells, or increased bc survival (and reduced apoptosis) in Alzheimer's CC patients. The beta-Trcp protein, and its active peptide fragments, or its CC nucleic acid, are used to screen for anti HIV-1 agents (antivirals), CC antitumour agents that disrupt cell cycle regulation or protein CC degradation in human tumour cells, and anti-inflammatory agents that CC disrupt activation by NFkappaB. Fragments of the protein are also CC useful for treating osteo-articular inflammation or acute inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 2151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2151 BP; 628 A; 467 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated with release of tumour necrosis factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human beta-transducin repeat containing protein and its fragments useful as, or to screen for, antiviral, antitumous
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30-JAN-1998;
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Polypeptide enhancing phosphorylated lkappaB ubiquitination useful for treating disorder associated with NF-kappaB activation e.g. cancer, comprising amino acid sequence of human E3 ubiquitin ligase or its
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CC which has been shown to have homology to human E3 ubiquitin ligase (E3). CC which has been shown to have homology to human E3 ubiquitin ligase (E3). CC E3 enhances ubiquitination of phosphorylated I-kappa-B, an inhibitor CC protein of nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B (CC degradation via the ubiquitin pathway is useful for identifying CC modulators of this process for use in treating diseases associated with CC extivation of NF-kappa-B. In vitro analysis suggests that deletion of CC the F-box results in a protein that functions as a dominant negative CC molecule in vivo. Transient over-expression of delta-beta-TrCP (a CC deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha CC in stimulated Jurkat cells, resulting in accumulation of phosphorylated CC in stimulated Jurkat cells, resulting in accumulations of NF-kappa-B CC activity. E3 and beta-TrCP can be used to screen for modulators of NF-kappa-B CC inflammatory diseases, autoimmune diseases, cancer and viral infections. Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

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03-FEB-1999;
15-MAR-1999;
          Chiaur
                                                                                                                                                                                                                                                               F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist; proliferative disorder; differentiative disorder; breast cancer; prostate cancer; ovarian cancer; cancer;
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                                                                                                  27-AUG-1999;
                                                                                                                                                                                                                                            inflammatory disorder; human;
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          Pagano M,
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99US-0118568.
99US-0124449.
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WPI; 2000-256635/22.
P-PSDB; AAY83041.
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Novel nucleic acid for screening compounds useful for treating proliferative and differentiative disorders such as cancer and disorders comprises sequences encoding ubiquitin ligases $\,$ immune

Disclosure; Figure 3b, 3c, 3d; 245pp; English.

Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases with F-box motifs (F-box proteins) are useful for diagnosis of proliferative and differentiated related disorders by measuring FBP gene expression. Cells expressing such proteins or their fragments are useful for screening compounds. The compounds are agonists or antagonists, which are useful for treating a proliferative or differentiative disorder in a mammal such as breast, ovarian and prostate cancer and small cell lung carcinoma and also major opportunistic infections, immune disorders, cardiovascular diseases and inflammatory disorders. FBP protein, analogs, derivatives and their subsequences, anti-FBP antibodies are also useful in diagnosis of the disorders.

Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

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RESULT
AAZ93710
ID AAZ9
XX AAZ9
AC AAZ9
XX IO-A
XX UDiq
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                                                      Claim 10;
                                                                                                                    Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with ubiquitin protein ligase or inhibiting ubiquitination using organic
                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-1998;
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»B; AAY83250.
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                                                                                    The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the cullin/ CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tunours, and in monitoring tunor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
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2041 ttttaaaco	961 gaatgcaagcgaattctcacaggccatacaggttcagtcctctgtctccagtatgatgag 1020	Db
	961	Qy
ш,	901 cagaaaatagtaagcggccttcgagacaacacaatcaagatctgggataaaaacacacattg 960 	Oy Db
gag		B 1
Oy 1921 tgagactcctgttg	781 aaaattatacaagacattiiriiriiriiriiriiriiriiriiriiriiriirii	Ov Db
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1621 cattco		Db
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QY 1561 gtggctgctttgg	y 481 cctatgttgcagagagatttcataactgctctgccagctcggggattggatcatatcgct 540 	Qy Db
1501	y 421 gaacatcttatatoccaaatgtgtoattaccaacatgggcacataaactcgtatcttaaa 480 	Оу
1441	y 361 aaggaactgtgtgtcaaatactttgagcagtggtcagagtcagatcaagtggaatttgtg 420 	ОУ
1381 tac	y 301 ggcacttccagtatgattgtgcccaagcaacggaaactctcagcaagctatgaaaaggaa 360 	Дb
		D 04
1261	y 181 aattoacitagacagacatacaacagctgtgccagactotgcttaaaccaagaaacagta 240 	ОУ
1201	y 121 teeteagagagagaagaetgtaataatggegaaeeeeetaggaagataataeeagagaag 180 	ОУ
1141	y 61 toggcgattatggacocggcogaggcggtgctgcaagagaaggcactcaagtttatgaat 120 	dd VQ
1081	1	da Qy
1021	Query Match 100.0%; Score 2151; DB 22; Length 2151; Best Local Similarity 100.0%; Pred. No. 0; Matches 2151; Conservative 0; Mismatches 0; Indels 0; Gaps	

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Matches 2136
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                                                                                                                                         be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the present or increased expression of the polynucleotide or the protein it encodes is useful for the diagnostis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ford
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them with genetically engineered vectors. Agonists or antagonists can be used in the treatment of cell proliferative and inflammatory disorders associated with decreased or increased CSIGP expression. CSIGP is used in the diagnosis, prevention and treatment of cell proliferative disorders like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory disorders like AIDS, Addison's disease, multiple sclerosis, etc.
                                                                                                                                   The present sequence is a cDNA obtained from Incyte clone 3239149 of COLAUCT01 library. It encodes cell signalling protein-12 (CSIGP-12). is expressed in musculo-skeletal, gastrointesinal and nervous tissues. Fragments of CSIGP encoding nucleic acid can be used as
Sequence
                                                                                                          hybridisation probe for detecting CSIGP related sequences or allelic variants. Recombinant CSIGP can be produced in host cells by transforming
                                                                                                                                                                                                         Claim 9; Page 87-88; 90pp; English.
                                                                                                                                                                                                                                       proliferative
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                                                cccctcctcctccttcacctctgcacctagttttttcccattggttccagacaaagg
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     marrow; antiinflammatory; cytostatic; neuropro
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide encoded by it are useful in the treatment of immune deficiencies and disorders. The deficiencies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 274-275; 648pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia;
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nes 2026; Conserv
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   03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
                                                                                                                                                                                                                                                                                                                                                                    vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell proliferation; cell differentiation;
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19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity in the diagnosis and/or activity in the diagnosis and or ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Liu C,
Zhao QA, Wang D,
Xue AJ, Yang Y,
                                                   Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 4584-4585; 6221pp; English
Sequence
                                                                                                                                                           treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic
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2000US-0663561.
2000US-0693325.
2000US-0728422.
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D, Wang J, Zh
Wejhrman T,
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, Zhang J, Ren
n T, Goodrich R;
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01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                            Tang YT,
Zhao QA,
Xue AJ, Y
                                                                                                                                                                                    05-FEB-2001;
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                                                                                                                                                                                                                                                                   vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                         30-NOV-2000;
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2000US-0560875.
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2000US-0620325.
2000US-062325.
2000US-063561.
2000US-063325.
2000US-0728422.
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Wang J, Zl
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2037	tgacctcatacttgcccaggacccattaaagtttgcggtatttaacgtatctgccaata	1978	Db
1850	tgacctcatacttgcccag	1792	Qy
1791	gaacccccccgttccccttctcgaacatacacctacatctccagataaataa	1732	Qy
1977		1918	Db
1731	agttcacatgatgacacaatcctcatctgggacttcctaaatgatccagctgcccaagct	1672	dq
1917		1858	Qy
1671	cttgtggagcattccggaagagtttttcgactacagtttgatgaattccagattgtcagt	1612	Qy
1857		1798	Db
1611	tgggatcttgtggctgctttggacccccgtgctcctgcagggacactctgtctacggacc	1552	Qy
1797		1738	Db
1551	tgtattcgatttgataacaagaggatagtcagtggggcctatgatggaaaaattaaagtg	1492	Qy
1737		1678	Db
1491	tgggacatagaatgtggtgcatgtttacgagtgttagaaggccatgaggaattggtgcgt	1432	Qу
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1431	tgtttgcagtacagggacaggctggtagtgagtggctcatctgacaacactatcagatta	1372	рь
1617		1558	
1371	tggaacacaagtacttgtgaatttgtaaggaccttaaatggacacaaacgaggcattgcc	1312	ду
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1311	gttgtagactttgatgacaagtacattgtttctgcatctggggatagaactataaaggta	1252	Qy
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1251	gcctccccaactgacattaccctccggagggtgctggtcggacaccgagctgctgtcaat	1192	Qy
1437		1378	Db
1191	ttcaataatggcatgatggtgacctgctccaaagatcgttccattgctgtatgggatatg	1132	Qy
1377		1318	Db
1131	aatacaggtgaaatgctaaacacgttgattcaccattgtgaagcagttctgcacttgcgt	1072	ФР
1317		1258	
1071	tatgatgagagagtgatcataacaggatcatcggattccacggtcagagtgtggggatgta	1012	Qy
1257		1198	Db
1011	aacacattggaatgcaagcgaattctcacaggccatacaggttcagtcctctgtctccag	952	Qy
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
             The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
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                                                                                                                                                                                                                                                                                                                                 ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin and is constituted by Skpl protein, Cull protein and a complex (SCF complex) of F-box protein containing F-box motif and WD40 repeat motif and has the amino acid sequence of 45 residues (AAB12811) or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1 protein) and (AAB12813, which is human beta-transducin repeat containing protein (beta-TTCP)). The F-box protein can be used for the gene therapy of colon cancer by being recombined to a virus vector. The present sequence encodes the human beta-TTCP protein from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F-box protein of ubiquitin ligase SCF complex which ubiquitination of IkappaB or beta-catenin \,\cdot\,
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gene therapy; colon cancer; beta-transducin repeat containing protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ubiquitin ligase SCF complex; F-box protein; ubiquitinatic
beta-catenin; Skpl; Cull; F-box motif; WD40 repeat motif;
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                                                                                                                                                                                                                                                                                                                         present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 17; 19pp; Japanese
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                                                        agacagacatacaacagctgtgccagactctgcttaaaccaagaaacagtatgtttagca
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01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
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                                                                      Zhao
                                                                              Tang YT,
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27-APR-2000;
                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene th
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
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                                                        Wang D,
Yang Y,
                                                                               Liu C,
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2000US-0560875.
2000US-9598075.
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nang J, Ren
Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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27-APR-2000;
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19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                          production of other cytokines in other cell populations. The polypuculeotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activinyinhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                               Sequence 2366 BP; 661 A; 519 C; 594 G; 592
                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to encode polypeptides (AAM78323-AAM80302) that exhibit activity elating to encode polynemia.
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                                                                                                                   112
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                                                      HYSEQ INC.
        Yang
       Liu C,
Wang D,
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2000US-0560875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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Search completed: May 11, 2002, 09:23:17 Job time: 11031 sec

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ALIGNMENTS

BASE COUNT	FEATURES Source	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 1 BE782628 LOCUS DEFINITION ACCESSION VERSION KEYWORDS
/db.xref="taxon: 9606" /db.xref="taxon: 9606" /clone="jMAGE:3868812" /clone="jMAGE:3868812" /clone="jMGCB7] /tissue_type="retinoblastoma" /tissue_type="retinoblastoma" /lab_host="DH108 (phage-resistant)" /note="Organ: eye; Vector: pcNV-SPORT6; Site_1: NotI; /note="Organ: eye; Vector: pcNV-SPORT6; Primer: Oligo dT. Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Site_2: Sali; Cloned unidirectionally constructed by Life Technologies." 193 a 156 c 175 g 185 t	Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9617 row: f column: 13 High quality sequence stop: 655. Location/Qualifiers 1. 709 //Organism="Homo sapiens"	human. Humoan sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 709) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: craphs-remail nih gov	BE782628 709 bp mRNA linear EST 20-OCT-2000 601465751F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868812 5', mRNA sequence. BE782628 BE782628.1 GI:10203826

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                                                                                                                                                                                                                                                                                                                                           actgcccagtttccctggactagccgaggagcagggctttgagactcctgttg 1934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAGCATTCCGGAAGAGTTTTTCGA 419
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                                                                                                                                                                                                                                                                                                                     AGTGGCCAGTTTCCCTGGACTAACCGAGGAGCCAGCGTTGGAGACTCCTGTGG
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                                                                                                                   Homo sapiens
                                                                                                                                                                                                   DKFZp434M1528_r1 434 (synonym: DKFZp434M1528 5', mRNA sequenc
Unpublished (1999)
              EST (Bloecker, et al.)
                                 Wiemann, S
                                            Bloecker, H., Boecher, M.,
                                                                                              Eukaryota; Metazoa; Chordata;
                                                                                                                                                       EST
                                                                                                                                                                                                                                         AL044095
                                                                                 Mammalia; Eutheria;
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                                                                                                                                                                                                   sequence
                                              Brandt, P., Mewes, H.W.,
                                                                                                                                                                                                                                     652 bp
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                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                     htes3) Homo
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                                              Gassenhuber, J.
                                                                                                                                                                                                                                   EST 29-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                      1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1599 ctgtctacggacccttgtggagcattccggaagagtttttcgactacagttttgatgaatt 1658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AAAAATTAAAGTGTGGGATCTTGTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                              atctgccaataccaggatgagcaacaacagtaacaatcaaactactgcccagtttccctg 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agctgcccaagctgaaccccccccgttccccttctcgaacatacacctacatctccagata 1778
                                                                                ccaggacggtctactcagcacaactgactgcttcagtgctgctatcagaagatgtcttct
                                                                                                                                                                                                                        GACTAGCCGAGGAGCAGGGCTTTGAGACTCCTGTTGGGACACAGTTGGTCTGCAGTCGGC
                                                                                                                                                                                                                                                gactagccgaggagcagggctttgagactcctgttgggacacagttggtctgcagtcggc 1958
                                                                                                                                                                                                                                                                                                       ATCTGCCAATACCAGGATGAGCAACAACAGTAACAATCAAACTACTGCCCAGTTTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                        AATAACCATACACTGACCTCATACTTGCCCAGGACCCATTAAAGTTGCGGTATTTAACGT
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                     cctagttttttcccattggttccagacaaaggtgacttataaatatatttagtg
                                                           CCAGGACGGTCTACTCAGCACAACTGACTGCTTCAGTGCTGCTATCAGAAGATGTCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCTGCCCAAGCTGAACACCCCCGTTCCCCTTCTCGAACATACACCTACATCTCCAGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTCTACGGACCCTTGTGGAGCATTCCGGAAGAGTTTTTCGACTACAGTTTGATGAATT 180
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone (DKFZp434M1528) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone from 5. Miemann, Polician Colone from Signature, Polician Research Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de; Research Centre for Biotechnology Ltd., sequenced by GBF (National Research Centre for Biotechnology Ltd., sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No si sequence available.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
/note="Vector: pSport1;
166 c 138 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="DKF2p434M1528"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.4e-164;
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  658 gtcaggacagattctctgtggagaggcctggcagaacgaagaggatgggggacagtattta 717
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                                                                                                                                                                                                                                                      ttcaaaaaccaaacctcctgacgggaatgctcctcccaactctttttatagagcactttat 777
                    ttggaatgcaagcgaattctcacaggccatacaggttcagtcctctgtctccagtatgat 1017
                                                                                               gatcagaaaatagtaagcggccttcgagacaacacaatcaagatctgggataaaaacaca 957
                                                                                                                                                                                                                                                                                                                                                                                          GTCCGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAGTATTTA 79
TTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAGTATGAT
                                                                           GATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACA
                                                                                                                                                                                                                               CCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGT 199
                                                                                                                                                                                                                                                                                                               TTCAAAAACCACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTAT 139
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AGENCOURT_6427660 NIH_MGC_67 Homo sapiens cDNA clone
5', mRNA sequence.
BM465280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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1 (bases 1 to 973)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone-"IMAGE:5502075"
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Pred. No. 1.3e-161;
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NIH MGC http://mgc.nci.nih.gov/.
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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             212
/clone_lib="NIH_MCC_17"
/tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="organ: muscle; Vector: pOTB7; Sites using the Directionally cloned into EcoRI/XhoI sites using the Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
12 a 149 c 202 g 195 t
                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match

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Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                    1 (bases 1 to 692)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
Unpublished (1999)
                                                                                                                                                                                                                                  BE269297 692 bp
601186356F1 NIH_MGC_8 Homo sapiens
                                          Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 692)
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                                                                                                        GCATGATGGTGACCTGGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGG-CTCCCCA
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM239 row: o column: 14
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/clone_lib="NIH_MGC_8"
/clone_lib="Nurkitt lymphoma"
/tissue_type="Burkitt lymphoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
02 a 134 c 179 g 177 t
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                                                                                                                                                                                                                                                                                112 tttatgaattcctcagagagagagactgtaataatggcgaaccccctaggaagataata 171
                                            292
                                                                                                                                                                                                                                                        188 TTCCAGAATTCCTCAGAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 247
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                                                                                                          gaaacagtatgtttagcaagcactgctatgaagactgagaattgtgtggccaaaacaaaa 291
CTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTAT
                                       cttgccaatggcacttccagtatgattgtgcccaagcaacggaaactctcagcaagctat 351
                                                                                      GAAACAGTATGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAA
                                                                                                                                                                          CCAGAGAAATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11451 row: h column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-*Organ: pooled brain, lung, testis; Vector: pcW-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RN source anonymous pool of 6 male brains, age range 23-27; male lung, age 27; and 1 male testis, age 69. Library i oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gruber (Invitrogen). Research Genetics tracking 021. Note: this is a NIH_MGC Library." a 187 c 215 g 185 t
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/db_xref="taxon:9606"
/clone="IMAGE:5180993"
/clone_lib="NIH_MGC_115"
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97.5%;
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1 (bases 1 to 743)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
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 Contact: Robert
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Strausberg, Ph.D
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654 aatggtcaggacagattctctgtggagaggcctggcagaacgaagagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 atgaattcctcagagagagacagactgtaataatggcgaaccccctaggaagataatacca 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaggaaaaggaactgtgtgtcaaatactttgagcagtggtcagagtcagatcaagtggaa 414
                                                                                                                                                  GTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAG
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                                                                                                                                                                                              gtgcaaggaatggtaccgagtgacctctgatggcatgctgtggaagaagcttatcgagag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTAAACCTATGTTGCAGAGAGATTTCATAACTTGCTCTGCCAGCTCGGGGATTGGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tttgtggaacatcttatatcccaaatgtgtcattaccaacatgggcacataaactcgtat 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCAATGGCACTTCCAGTATGATTGTGCCCCAAGCAACGGAAACTCTCAGCAAGCTATGAA 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ntund chaves, the property of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/lab_host="pH108"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: SalI-XhoI (gtcgag pBluescript Translated using primary size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

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/db_xref="taxon:9606"
/clone="IMAGE:4825970"
/clone_lib="NIH_MGC_97"
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98.8%;
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Pred. No. 1.7e-145;
Pred. No. 1.7e-6;
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TITLE
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Best Local 9
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364 gaactgtgtgtcaaatactttgagcagtggtcagagtcagatcaagtgg-aatttgtgga 422
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                                       tagcaagcactgctatgaagactgagaattgtgtggccaaaacaaaacttgccaatggca 304
                                                                                                                                                                                                    CACTTAGACAGACTTACAACAGCTGTGCCAGGCTTTGCATAAACCAAGAGACAGTATGTC 180
                                                                                                                                                                                                                       cacttagacagacatacaacagctgtgccagactctgcttaaaccaagaaacagtatgtt 244

        cagagagagactgtaataatggcgaaccccctaggaagataataccagagaagaatt
        184

                                                                                                                                                                                                                                                                                                                                                                                     cgattatggacccggccgaggcggtgctgcaagagaaggcactcaagtttatgaattcct 124
                                                                                                                         TAACAAGCACTGCTATGAAGACTGAAAATTGTGTGGCCAAAGCCAAACTTGCCAATGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG518761
BG518761.1 GI:13513945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 587.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo: Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

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/strain="CZECH II (feral)"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:3491843"
/clone_lib="NCI_CGAP_Lu29"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 534.4; DB 10
Pred. No. 1.2e-136;
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 637)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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//db_xref="rvB/N"
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not in the second of the se
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Clone from S. Wiemann, Molecular Genome Analysis,
          Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 3' sequence of the clone insert
                                                                    EST (Bloecker, et al.)
Unpublished (1999)
                                                                                            Wiemann, S
                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 544)
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AL041438.1 GI:5420789
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                                                        Contact: Bloecker H
                                                                                                         Bloecker, H., Boecher, M., Brandt, P.,
                                                                                                                                                                     Homo sapiens
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                                                                                                            Gassenhuber, J.
German
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RESULT 12
BI455545
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DEFINITION

ACCESSION

mRNA sequence BI455545

603173974F1 NCI_CGAP_Mam5 Mus

dq 888

mRNA

linear

musculus cDNA clone IMAGE:5253090

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                                                                                  2063 tcctttcacctctgcacctagttttttcccattggttccagacaaaggtgacttataaat 2122
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                                                                                                                                                   | tcagaagatgtcttctatcaattgtgaatgattggaacttttaaacctcccctcccctctcc
                                                                                                                                                                                                                                                                      ctgcccagtttccctggactagccgaggagcagggctttgagactcctgttgggacacag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tacagtttgatgaattccagattgtcagtagttcacatgatgacacaatcctcatctggg 1702
ATATT 1
                                                                   TCCTTTCACCTCTGCACCTAGTTTTTCCCATTGGTTCCAGACAAAGGTGACTTATAAAT
                                                                                                                                     TCAGAAGATGTCTTCTATCTTTTGTGAATTGGAACTTTTAAACCTCCCCTCCTCCTCC
                                                                                                                                                                                                     ttgcggtatttaacgtatctgccaataccaggatgagcaacaacagtaacaatcaaacta 1882
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                                                                                                                                                                                                                                    cctacatctccagataaataaccatacactgacctcatacttgcccaggacccattaaag 1822
                                                                                                                                                                                                                                                                                                                                         TTGCGGTATTTAACGTATCTGCCAATACCAGGATGAGCAACAACAGTAACAATCAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                           CCTACATCTCCAGATAAATAACCATACACTGACCTCATACTTGCCCAGGACCCATTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone (DKFZp434D2317) is available at the RZPD in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          German Genome Project
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/clone_lib="434 (synonym:
/tissue_type="testis"
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102 c 153 g 138 t
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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99.4%;
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Pred. No. 1.9e-135;
0; Mismatches 2;
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CTCAGGAGGGTGCTGGGGACACCGAGCTGCGGTCAATGTTGTAGACTTTGATGACAAG 420
                      ctccggagggtgctggtcggacaccgagctgctgttcaatgttgtagactttgatgacaag
                                                                                                 acctgctccaaagatcgttccattgctgtatgggatatggcctccccaactgacattacc
                                                                                                                                                      CATTGATTCACCACTGTGAAGGCCGTTCTGCACCTGCGCTTCAATAATGGCATGATGGTG
                                                                                                                                                                          cgttgattcaccattgtgaa-gcagttctgcacttgcgtttcaataatggcattgatggtg 1152
                                                                                                                                                                                                                                   CAGGCTCCTCAGACTCCACCGTCAGAGTGTGGGATGTAAATGCAGGTGAGATGCTAAACA
                                                                                                                                                                                                                                                       GCGGCCTTCGAGACAACACCATCAAGATCTGGGATAAAAGCACACTGGAATGCAAGCGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                              gcggccttcgagacaacacaatcaagatctgggataaaaacacattggaatgcaagcgaa 973
                                                                                                                                                                                                                                                                                                              TTCTCACGGGCCACACGGGCTCCGTCCTGTGTCTGCAGTACGATGAGAGGGTGATCATCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGGAGTGAAACAAGTAAAGGGGTTTACTGTTTACAGTACGACGACCAGAAGATAGTCA 60
                                                                           ACCTGTTCCAAAGACCGTTCCATCGCTGTGTGGGATATGGCTTCCCCAACTGACATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 5 High quality sequence stop: 684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11639 row: d column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal: Site_2: NotI; Cloned unidirectionally. Primer: Oligo di Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db.xref="taxon:10090"
/clone="IMAGE:5253090"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57/B6"
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                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
Other_ESTs: H3073A06-3
Contact: George J. Kargul
                                                                                                                                                                                                                       Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the
visit http://lgsun.grc.nia.nih.gov/cDNa/15k.html f.
Plate: H3073 row: A column: 06
Seq primer: -21M13 Reverse
High quality sequence stop: 646
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H3073A06-5 NIA Mouse 15K cDNA Clone
H3073A06 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Ja,T.S., Carter,M.G. and Ko,M.S.H.
Verification and initial annotation of NIA mouse
                                                                                                                                                                                                            POLYA=No
                                                                                                                                                                                                                                                                                                                                              333 Cassell Drive, Suite 4000, Baltimore,
                                                                                                                                                                                                                                                                                                                                                                   National Institute on Aging/National Institutes of Health
                                                                                                                                                                                                                                                                                                                                                                                             Laboratory of Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
                                                           /db_xref="niaEST:H3073A06-5"
/db_xref="taxon:10090"
/clone="H3073A06"
                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                Location/Qualifiers
                                                                                                                         /strain="C57BL/6J"
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Best Local Similarity
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602 TGCTCCAGCAGGGACTCTCTGTGTGGGGACACTTGTGAAGCA 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           982 ggccatacaggttcagtcctctgtctccagtatgatgagagagtgatcataacaggatca 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgctcctgcagggacactctgtctacggacccttgtggagca 1622
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                                                                                                                                                                                                                                                                                   AGTGTTGGAGGGCCATGAGGAGTTGGTACGCTGCATTCGATTTGATAACAAAAGGATAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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1843 gccaataccaggatgagcaacaacagtaacaatcaaactactgcccagtttccctggact
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                                                                                                                                            GCACAAGCTGAACCCGCCCGTTCCCCTTCTCGAACAGACACCTACATCTCCAGATAAATA
                                                                                                                                                                              gcccaagctgaacccccccgttccccttctcgaacatacacctacatctccagataaata 1782
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541 bp mRNA linear EST 25-JAN-2001
naf16h04.x1 Soares_NPBMC Homo sapiens cDNA clone IMAGE:4141302 3'
similar to TR:09Y213 09Y213 BETA-TRANSDUCIN REPEATS CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    info@image.llnl.gov
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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BG058605.1 GI:12525270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Toloned into the Not I and Eco RI sites of the modified pTT3 vector. Library is normalized; constructed in the laboratory of M. Bento Soares (University of Iowa)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="lymphocyte"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pT7T3D-Pac; Site_1: NotI;
Site_2: EcoRI; 1st strand cDNA was primed with a Not I -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4141302"
/clone_lib="Soares_NPBMC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                             22.9%;
95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 492.2; DB Pred. No. 5e-125;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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BASE COUNT
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AW762522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                      Seq p
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW762522 590 bp mRNA linear EST 04-MAY 1 MAGE: 3155000 Similar to TR:Q9Z159 Q9Z159 BETA-TRANSDUCIN REPEAT CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                MGI:1057762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_ESTs: ur63g08.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia;
1 (bases 1 to 590)
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                   169 a
                                                                                                                                                                                                                                                                                                                                                                                        primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 428
Location/Qualifiers
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetic: 22, 37-43 (1999)."

3 138 c 149 g 132 t 2 others
                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:3155006"
                                                                                                                                                             /lab_host="DH10B"
                                                                                                                                                                            /tissue_type="tumor, gross tissue"
/dev_stage="10 months"
                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Mam3"
                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="129 - C57/B6 - FVBN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp mRNA linear EST 04-MAY-2000 musculus cDNA clone IMAGE:3155006 5'
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                                         Xu et al., Nature Genetics
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                  806 tagaatotaattggagatgtggaagacatagtttacagagaattcactgc 855
541 TAGAGTCCAATTGGAGATGTGGGCGACATNAGTTACAGAAGATCCACTGC 590
                                                                                                                                     421
                                                                                                                                                                                        361 GCATGCTGTGGAAAAAGCTCATCGAGAGGATGGTCANGACGGACTCTCTGTGGCGAGGCC
                                                                                                                                                                                                                                  626
                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                               566
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                                                           CTCCTCCCAACTCCTTTTATAGAGCGCTTTATCCTAAAATCATACAAGACATTGAGACAA 540
                                                                                  otcotcocaactctttttatagagcactttatcctaaaattatacaagacattgagacaa
                                                                                                                           tggcagaacgaagaggatggggacagtatttattcaaaaaccaaacctcctgacgggaatg
                                                                                                                                                                                                            gcatgctgtggaagaagcttatcgagagaatggtcaggacagattctctgtgtggagaggcc
                                                                                                                                                                                                                                                   CCAAGTCACTGTGTGCTGAGCTCGTGTGCAAGGAATGGTACCGCGTGACGTCGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCAGCGGAAACTCTCAGCAAGCTATGAGAAGGAAAAGGAGCTGTGTGTCAAGTATTTTG 120
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89.2%;
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Pred. No. 4.6e-124;
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Search completed: May 11, 2002, 08:40:06 Job time: 13285 sec

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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SPTREMBL_17:+

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate
6: sp_mamnal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate
14: sp_unclassifi
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Gapop 10.0 , Gapext 0.5
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3034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                         sp_organelle:*
sp_phage:*
                                                                                                                                                                   sp_invertebrate:*
sp_vertebrate:*
sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	% Query Match Length DB	BB	ID	Description
ב	2997	98.8	569	11	Q9QUI5	Q9qui5 mus musculu
2	2990	98.5	569	11	Q9Z159	Q9z159 mus musculu
ω	2978	98.2	569	11	Q9R1G7	Q9r1g7 mus musculu
4	2089.5	68.9	510	ഗ	044382	044382 drosophila
ر ت	2089.5	68.9	510	ഗ	Q9VDE3	Q9vde3 drosophila
σ,	1638.5	54.0	665	Ç,	Q9GNN6	Q9gnn6 caenorhabd
7	1498	49.4	430	ហ	Q9вJ54	Q9bj54 heterodera
8	690	22.7	506	ω	Q9P7V1	Q9p7v1 schizosacch
9	661	21.8	1326	Çī	Q9VZF4	Q9vzf4 drosophila
10	640	21.1	553	4	Q9NUX6	Q9nux6 homo sapien
11	520	17.1	587	Çī	044083	O44083 caenorhabd:
12	387.5	12.8	304	11	Q9D4T2	Q9d4t2 mus muscui
13	365.5	12.0	942	ۍ	096611	096611 dictyosteli
14	356	11.7	410	13	Q9PTR5	Q9ptr5 gallus gal
15	351	11.6	410	6	Q9GL51	Q9g151 sus scrofa
16	344	11.3	411	5	869960	096698 drosophila
17	339.5	11.2	777	ω	Q9USN3	Q9usn3 schizosacch
18	334.5	11.0	283	11	Q99JV3	Q99jv3 mus musculı
19	334.5	11.0	454	4	004400	001-00 1-1-1-1-1

444444 336 337 344 444 444 444 444 444 444 444 444
3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
110.9 110.9 110.9 110.7 110.7 110.7 110.3 110.3 110.3 110.3 110.3 110.3 110.3 110.3 110.3 110.3 110.3 110.3 110.3 110.9 9.8 9.9 9.8 9.8 9.8 9.8 9.8 9.8 9.8 9
317 454 594 333 331 3277 3277 331 481 487 487 487 487 487 1205
110 110 1110 11111 11111 11111 11111 11111 11111 1111
Q9MZZZ Q9QUH1 Q9HQ73 Q9SYQ0 Q9RZA6 Q35592 Q9D7H2 Q9LPR4 Q9LPR4 Q9LPE2 Q9BU54 Q9LFE2 Q9BU54 Q9LFE2 Q9BU55 Q9LFE2 Q9BU55 Q9LFE2 Q9BU55 Q9LFE2 Q9BU55 Q9LFE2 Q9BU55 Q9LFE2 Q9BU56 Q9LFE2 Q9BU56 Q9BU56 Q9BU56 Q9BU56 Q9BU58 Q9
O9m2z2 arabidopsis O9quhl mus musculu O9h073 homo sapien O9sy00 arabidopsis O9r2a6 mus musculu O35592 mus musculu O9d7h2 mus musculu O9d7h2 mus musculu O9d7h2 mus musculu O9h054 homo sapien O9h054 homo sapien O9h054 homo sapien O9h162 arabidopsis O96995 drosophila O9uj66 homo sapien O9uj65 homo sapien O9uj67 homo sapien O9uj68 homo sapien O9uj68 homo sapien O9uj68 homo sapien O9uj69 homo sapien O9uj64 homo sapien O9uj63 homo sapien O9uj63 homo sapien O9uj64 homo sapien O9uj65 homo sapien O9uj66 homo sapien O9uj67 homo sapien O9uj68 schlzosacch O9uj68 homo sapien O9uj69 homo sapien O9uj68 homo sapien

ALIGNMENTS

RP RA DR DR DR DR DR	R R R R R R R R R R R R R R R R R R R	RESULT Q9QUI5 ID Q0 AC Q0 DT Q0 DT Q0 DT Q0
SEQUENCE FROM N.A. Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF081887; AAD107755.1; EMBL; AF099932; AAD08701.1; EMBL; BC00399; AAH03999.1; MGD; MG1:1338871; Btrc. InterPro; IPR001810; F-box. InterPro; IPR001680; WD40. Pfam; PF00646; F-box; 1. Pfam; PF00640; WD40; 7.	SEQUENCE FROM N. A. SEQUENCE FROM N. A. MEDLINE-99199275; PubMed-10097128; Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M., Hattori K., Higashi H., Nakano H., Okumura K., Once K., Good R.A., Nakayama Ki.; "Ubiquitin dependent degradation of IkappaBalpha is mediated by a ubiquitin ligase Skpl/Cul 1/F-box protein FWDl."; Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999). [2] SEQUENCE FROM N.A. MEDLINE-99075339; PubMed-9859996; Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M., Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.; "Identification of the receptor component of the IkappaBalpha- ubiquitin ligase"; Nature 396:590-594(1998).	LT 1 15 19QUI5 PRELIMINARY; PRT; 569 AA. 9QUII5; Ol-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 01-JUN-2001 (TREMBLREL 17, Last annotation update) UBIQUITIN LIGASE FWD1 (BETA-TRANSDUCIN REPEAT CONTAINING PROTEIN). BTRC. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090;

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R PROSITE; PS50181; FBOX; 1.

R PROSITE; PS500818; WD_REPEATS_1; UNKNOWN_6.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

Ligase; Repeat; WD repeat.

SEQUIPMORE FOR THE PROSITE PS50294; WD_REPEATS_REGION; 1.
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Best Local Similarity
Matches 561; Conserv
                                                              BTRC.
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eukaryota; Butheria; Rodentia;
                                                                                                                     O9Z159;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-TRANSDUCIN REPEAT CONTAINING PROTEIN.
SEQUENCE FROM N.A. MEDLINE=99145465; Spencer E., Jiang
                                                                                                                                                                                              Q9Z159
                                                         NCBI_TaxID=10090;
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569 AA; 65105 MW; BC7D6544815B2296 CRC64;
                                                                                                                                                                                              PRELIMINARY;
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 PubMed=9990853;
J., Chen Z.J.;
                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
SMART; SM00320; WD40; 7.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS50678; WD_REPEATS_1; UNKNOWN_6.
PROSITE; PS50082; WD_REPEATS_REGION; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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EMBL; AF112979; AAD04181.1;
MGD; MGI:1338871; Btrc.
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InterPro; IPR001680; WD40.
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569 AA; 65047 MW; BC7C7A44815BED96 CRC64;
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Pred. No. 1.9e-238;
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Best Local Similarity
Matches 557; Conserv
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Submitted (DEC-1998) to the E
EMBL; AF110396; AAD41025.1; -
InterPro; IPR001810; F-box.
InterPro; IPR001880; WD40.
Pfam; PF00646; F-box; IPR0186; PF00846; P-box J.
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SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
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Mammalia; Eutheria;
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aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                     ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                        VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
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                                                                  ILIWDFLNDPAAHAEPPRSPSRTYTYISR
                                                                                                                            KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                                                                          EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 480
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                                                                                                                 KRIVSGRYDGKIKVWDLMAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                                                              EFYRTLNGHKRGIACLQYRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
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          PRELIMINARY;
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Pred. No. 1.9e
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Best Local Similarity
Matches 394; Conserv
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01-JUN-1998
01-JUN-2001
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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SMART; SM00250; WD40; 7.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

REPEATS_PS50294; WD_REPEATS_REGION; 1.

SEQUENCE 510 AA; 58952 MW; DBB0243D373
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InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
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DTILIWDFLNFTPNENKTGRTPS
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                        DTILIWDFLNDPAAQAEPPRSPS
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RESUDER OF SECOND PERSON OF SECOND PERSO
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"The genome sequence of Drosophila melanogaster.";

Excenter of the sequence of Drosophila melanogaster.";
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01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
SLMB PROTEIN (SLIMB).
                                                                                                                                                                           Miletich I., Limbourg-Bouchon B.;
"Drosophila null slimb clones transiently deregulate Hedgehog-
independent transcription of wingless in all limb discs, and induce
decapentaplegic transcription linked to imaginal disc regeneration.";
Mech. Dev. 93:5-26(2000).
EMBL; AE00373; AAF558531; -.
EMBL; AF222924; AAF63214.1; -.
EMBL; AF222924; AAF63213.1; -.
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NCBI_TaxID=7227;
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Eukaryota; Metazoa; Arthropoda; Trac
                                             InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                            FlyBase; FBgn0023423; slmb.
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Best Local
                                                                                                                                                                                    01-MAR-2001
01-MAR-2001
01-JUN-2001
                         PubMed=11060233;
Kipreos E.T., Gohel S.P., Hedgecock E.M.;
"The Caenorhabditis elegans F-box/MD-repeat protein LIN-23 functions
to limit cell division during de Development 127:5071-5082(2000).
                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                        LIN-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; |
SEQUENCE
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PROSITE; PS00678; WD_REPEATS_1; 5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                            LIN-23
                                                                                                                                                                                                                                Q9GNN6;
                                                                                                                                                                                                                                             Q9GNN6
                                                                      SEQUENCE FROM N.A.
                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00256; FBOX; SMART; SM00320; WD40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
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                                                                                                                                                                                                                                                                                                                   DTILIWDFLNFTPNENKTGRTPS
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                                                                                                                                                                                                                                                                                                                                                                        DTKRIVSGAYDGKIKVWDLVAALDPRAASNTLCLNTLVEHTGRVFRLQFDEFQIVSSSHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNSIRLWDIECGACLRVLEGHEELVRCIRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVKTLMGHTGSVLCLQYDDKVIISGSSDSTVRVMDVNTGEMVNTLIHHCEAVLHLRFNNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METDKIMDETN-SNAQAFTTTMLYDPVRKKDSSPTYQTERELCFQYFTQWSESGQVDFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WD repeat.
E 510 AA;
                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                             PRELIMINARY;
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78.3%;
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16,
17,
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                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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Pred. No. 3.4
              development."
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SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
SMART; SM00320; WD40; 7.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; WD repeat. SEQUENCE 665 AA; 75916 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF275253; AAG28037.1;
                                                                                                                            Q9BJ54:
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN (FRAGMENT).
                                                                             Heterodera glycines.
Eukaryota; Metazoa; Nematoda; Chromadorea; '
Tylenchoidea; Heteroderidae; Heteroderinae;
                                                                                                                                                                                                             Q9BJ54
SEQUENCE FROM N.A.
Kovaleva E.S., Yakovlev A
"Plant parasitic nematode
                                                                NCBI_TaxID=51029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPA----HLVELILFNVNSDSLKSCEEVSTSWRCALARGQHWKKLIEKNVRSDSLWWGLS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLA 207
                                                                                                                                                                                                                                                                                          DAP-----PSGLPSST 513
                                                                                                                                                                                                                                                                                                                                                                                                                   SIAVWDWASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLN 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSVLCLQYDNRVIISGSSDATVRVWDVETGECIKTLIHHCEAVLHLRFANGIMVTCSKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDR 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNWKRGNYKMTRINCQSENSKGVYCLQYDDDKIVSGLRDNTIKIWDRKDYSCSRILSGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKRQWDKFLNISRDMSVRRICEKFNYDVNIKRDKLDQLILMHVFYSKLYPKIIRDIHNID
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                                                                                                                                                                                                                                                                                                                      NDPAAQAEPPRSPSRT 563
                                                                                                                                                                                                                                                                                                                                                     YDGKIKVWDLQAALDPRALSSEICLCSLVQHTGRVFRLQFDDFQIVSSSHDDTILIWDFL
                                                                                                                                                                                                                                                                                                                                                                    YDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                             GHKRGIACLQYRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIAVWDMVSPRDITIRRVLVGHRAAVNVVDFDDRYIVSASGDRTIKVWSMDTLEFVRTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERRGWGQYL---------FKNKPPDGNAPPNSFYRALYPKIIQDIETIE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.0%; Score 1638.5; DB 5; 63.7%; Pred. No. 8.1e-127; tive 59; Mismatches 92;
   b-TRCP
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                   Masler
                                                                                                Chromadorea; Tylenchida;
                   E.P.;
                                                                                                                                                                                                             430 AA
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                                                                                                 Tylenchina;
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Pfam; PF00646; F-box; 1.

Pfam; PF00640; WD40; 7.

PRINTS; PR00320; GPROTEINBRPT.

SMART; SM00256; FBOX; 1.

SMART; SM00250; WD40; 7.

PROSITE; PS50181; FBOX; 1.

PROSITE; PS50082; WD_REPEATS_1; UNKNOWN_3.

PROSITE; PS50082; WD_REPEATS_2; 6.

PROSITE; PS50082; WD_REPEATS_2; 6.

PROSITE; PS50082; WD_REPEATS_1.

PROSITE; PS50082; WD_REPEATS_1.

PROSITE; PS50082; WD_REPEATS_1.

Repeat; WD repeat.

SEQUENCE 506 AA; 58256 MW; CEF34D4EFFBC21
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                                                                                                                                                                                                                                                                                                                                     McDougall R.C., Rajandream M.A., Barrell B.G., Brown S. Jones L., McNeil A., Harris D.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL136538; CAB66464.1; -. InterPro; IPR001810; F-Dox. InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9P7V1;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPAC30.05.
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WD-REPEAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9P7V1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDDTILIWDFLN-DPAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDDTILIWDFLNTGPSAAVAAGAAAAAHNQAVQHHQAAPAAQPA 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QAEPPRSPS 561
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            CEF34D4EFFBC2E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barrell B.G., Brown S., Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506
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Ouery Match Best Local Similarity

Length 506;

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9VZF4:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
CG15010 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VZF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 QMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 KNVVSKVSDLTSCSDFSTSSPVPCLNPLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNGKFIVSGSSDLTIRIFEASSGKLLRMLQGHEDLIRTVRFNDEKIVSGGYDGTVRIWN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITLRRVLVGHRAAVNVVDFDDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAALDPRAPAGTLCLRTLVEH-----SGRVFRLQFDEFQIVSSSHDDTILIWDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVW--DMASPTD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RATLDSVYCVQYDDEIMVSGSKDRTVSVWDVNSRFILYKLYGHSGSVLCLDFCRRRNLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VII 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEDPGIWKALYMQKGWFVNENVLNEFEAWRRTHKFPQPRFENFLKQQNIIGPYGTMFLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLSKEGVVAVYNHVRSLLFTDFTEVFP----EEVSLRVFSYLDQLDLCKCKLMSKRWKRL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACM-HVLRGHLASVNSVQYSSKTGLIVTASSDRTLRTWDITTGHCIRIIHAHQRGIACAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSSDSTIIIWDWQNRRPLKVYFGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFIF-----DSNGRPLLNWSYLY----KEHAHLDSNWRHGRFLVSTFNNPSIRFPADQDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---FNTGEQHCVLHNSRNSRVFGLQFDHRRIIACTHSSEILVWNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.7%; Score 690; DB 3; 30.4%; Pred. No. 1.1e-48; tive 104; Mismatches 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1326 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Doddson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Duddson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Duddson K.J., Evangelista C.C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heimann T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mental S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylera E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Waillams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
RT "The genome sequence of Drosophila melanogaster.";
RI Science 287.2185-2195,2000).
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PROSITE; PS50182; WD_REPEATS_1; 5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

Repeat; WD repeat.

SEQUENCE 1326 AA; 141360 MW; 3F42C873CFA3027F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00320; GPROTEINBRPT SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00646; F-box; Pfam; PF00400; WD40;
                  456 DIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003480; AAG22246.1; FlyBase; FBgn0035516; CG150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:2185-2195(2000):
                                                                                                                                                                                                                                                                                                                                            954
                                                                                                                                                                                                                                                                                                                                                                                                                                908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 852 FQRWSHVERLLALDRLIDHCDPSQVRHMMKVIEPQFQRDFISLLPR----ELALFVLSYL 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 FEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 DAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPP-- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                             VQYDGKLIVSGAYDYMVKIWHPERQECLHTLQGHTNRVYSLQFDGLHVVSGSLDTSIRVW
                                                                                                                                                                                            TGEMLNTLIHHCEAVLHLRFNNGMMYTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV
                                                                                                                                                                                                                                           SGNRIVSGSDDNTLKVWSAVNGKCLRTLVGHTGGVWSSQMSGNIIISGSTDRTLKVWDMD
                                                                                                          VDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLW
                                                                                                                                                      SGACVHTLQGHTSTVRCMHLHGSKVVSGSRDATLRVWDIEQGSCL---HVLVGHLAAVRC 1120
                                                                                                                                                                                                                                                                       DDQKIYSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTYRVWDVN 335
                                                                                                                                                                                                                                                                                                                                  RDGNMPPIASPWKAAYMR---QHI--IEMNWR-----SRPVRKPKVLKGHDDHVITCLQF
                                                                                                                                                                                                                                                                                                                                                                               -DGNAPP-NSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKG-----VYCLQY 275
                                                                                                                                                                                                                                                                                                                                                                                                                            EPKDLLRAAQTCRSWRFLCDDNLLWKEKCRKA-----QILAEPR-----SDRPKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
21.8%; Score 661; DB 5; 34.9%; Pred. No. 9.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG15010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu Nakamura Y., Nagahari K., Masuho Y., Sasaki N.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AK001933; BAA91986.1; -InterPro; IPR001810; F-box.
InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00256; FBOX; 1.
SMART; SM00320; WDA0; 7.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TremBLrel. 15, Created)
01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
CDNA FLJ11071 FIS, CLONE PLACE1004937, MODERATELY SIMILAR TO SEL-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; WD repeat.
SEQUENCE 553 AA; 62280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00646; F-box; 1.
Pfam; PF00400; WD40; 7.
PRINTS; PR00320; GPROTEINBRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NUX6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9NUX6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1181 DVETGNCKHTLMGHQSLTSGMELRQNILVSGNADSTVKVWDITTG-----QCLQTL 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1232
                                                                                                                                                 170
                                         307
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                                                                                                                                                                                                                                                                                                                               74
                                                                                                                                                                                                                                                                                                                                                                                         14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD
                                                                 DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                                                         ESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH
                                                                                                                                          KCKE-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                                                                                                          LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIODIETI 246
                                                                                                                                                                                                             MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE
                                                                                                                                                                                                                                                                                  RAANGQG-----QQRRRITSVQPPTGLQEWLKNFQSWSGPEKLLALDELIDSCEPTQVKH 113
                                                                                                                                                                                                                                                                                                                    KLANGTSSMIVPKQRKLSASYEKEKEL--CVKYFEQWSESDQVEFVEHLISQMCHYQHGH 131
                             TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD
                                                                                                                                                                                                                                                  INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
                                                                                                                                                                                                                                                                                                                                                         KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGPNKHHSAVTCLQFNSRFVVTSSDDGTVKLWD 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V---EHSGRVFRLQFDEFQIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                        167;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                              21.1%; Score 640; DB 4; I
30.8%; Pred. No. 1.6e-44;
tive 92; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA829C221986A3F2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                72;
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                                 366
                                                                     266
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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01-JUN-1998
01-JUN-1998
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50294; WD_REPEATS_REGION; 1.
Repeat; WD repeat.
SEQUENCE 587 AA; 65311 MW; 2D3970B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00890; ABC2_MEMBRANE; UNKNOWN_1.
PROSITE; PS00618; FDX; 1.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
PROSITE; PS0082; WD_REPEATS_2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00320; GPROTEINBRPT SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "sel-10, a negative regulator of lin-12 activity in Caenorhabditis elegans, encodes a member of the CDC4 family of proteins."; Genes Dev. 11:3182-3193(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-98051191; PubMed-9389650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00646; F-box; Pfam; PF00400; WD40; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000412; ABC2_transport.
InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF020788; AAC47809
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                       228 PN-SFYRALYPKIIQDI-----
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                                                                                                                                                                                                                                                                                                                       35
                                                                                                                                                                                                                                                                                                                                                                       72 KTKLANGTSSMI------VPKQRK--LSASYEKEKEL-----CVKYFEQWSESDQVE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                SKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAIAAG-----VTIPDHIQP
                                                                                                                                         CKEWYRVTSDGMLWKKL-IERMV-----RTDSLWRGLAERRGWGQYLFKNKPPDGNAP
                                                                                                                                                                                                                                                     FVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELV
                                                                                                                                                                                               AFTRLLQESNMTNIRQLRAIIEPHFQRDFLSCLPV----ELGMKILHNLTGYDLLKVAQV
                                                                                                                                                                                                                                                                                                                 ESSYSNGSSSSYNADKLSSSRPLQHKLDLSASPSRNNDLNPRVEHLIALFKDLSSAEQMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 (TrEMBLrel.
9 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.1%;
28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06,
06,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                78; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2D3970B4EFAA1B8C CRC64;
                       --ETIESNWRCGRHSLQRIHCRSETSKGVYCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   70;
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                  150
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                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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Query Match

DB 11;

Length

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Arakawa T., Saito R., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bullt C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
4930563E19RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).

Mus musculus (Motazoa; Chordata;
                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=TESTIS; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9D4T2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9D4T2
                                                                                                                                                                   MGD; MGI:1923089; 4930563E19Rik.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                            Nature 409:685-690(2001).
EMBL; AK016201; BAB30146.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4930563E19RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel.
                                        PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                          PRINTS; PR00320; GPROTEINBRPT.
                                                                                                                                                  Pfam; PF00400; WD40;
                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection ";
                                                                                                                                                                                                                                                                        Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 CDLNVHRFLKLQKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIHDDVLVTGSDDNTLKVWCIDKGEVMYTLVGHTGGVWTSQISQCGRYIVSGSTDRTVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTIRLWDI----ECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVRCVQFDGTTVVSGGYDFTVKIWNAHTGRCIRTLTGHNNRVYSLLFESERSIVCSGSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSTVDGSLLHTLQGHTSTVRCMAMAGSILVTGSRDTTLRVWDVESGRHLA---TLHGHHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSIRVWDFTRPEGQECVALLQGHTSLTSGMQLRGNILVSCNADSHVRVWDI-------H
                                                                                                         SM00320; WD40;
                         WD repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
        33173 MW; AFAACDC487939E3D CRC64;
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17,
17,
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304
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 096611
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PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                              "A novel, putative MEK kinase controls developmental timing and spatial patterning in Dictyostelium and is regulated by ubiquit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096611
                                                                                                                                                                                                                                                               -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES EMBL; AF093689; AAC97114.1; -. InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                           Genes Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999
01-JUN-2001
                                                                                          SMART;
                                                                                                                   SMART;
                                                                                                                                 PRINTS; PR00109;
                                                                                                                                                           Pfam; PF00069; pkinase; 1. Pfam; PF00400; WD40; 7.
                                                                                                                                                                                      Pfam; PF00646; F-box;
                                                                                                                                                                                                                                                                                                        mediated protein degradation."; Genes Dev. 12:3564-3578(1998).
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99051319; PubMed=9832508;
Chung C.Y., Reddy T.B.K., Zhou K., Firtel R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999
                                     PROSITE; PS00107; PROSITE; PS50011;
                                                                             SMART;
                                                                                                        SMART;
                                                                                                                                               PRINTS;
                                                                                                                                                                                                 InterPro; IPR001245; Tyr_k
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                           InterPro; IPR002290;
                                                                                                                                                                                                                                      InterPro; IPR001810;
InterPro; IPR000270;
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-KAX-3
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEK KINASE ALPHA.
                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 IW 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 YDER--VIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG--MMVTCSKDRSIA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 QRIHCRSETSKGYYCLQYDD----QKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 IW 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 TGSSDKTARIWDVQTG------QCLQVLEGHTDEIFSCAFNYKGNIVITGSKDNSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 BELHTLEGHKNVVYAIAFNNPYGDKIATGSFDKTCKLWSAETGKCYHTFRGHTAEIVCLS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VWDMASPTDITLRRVLVGHRAAVN--VVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNPQSTVVATGSMDTTAKLWDIQNGEEVVTLTGHLAEIISLSFDTSGDRIITGSFDHTVV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQ--IVSSSHDDTIL 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDDEILDSCFDYTGKLIATASADGTARVYNATTRKCVTKLEGHEGEISKISFNPQGNRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HKRGI--ACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFD--NKRIV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWDASTGRKV---HTLIGHCAEISSALFNWDCSLILTGSMDKTCMLWDATSGKYVATLTG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                 SM00220; S_TKc; 1.
SM00320; WD40; 7.
E; PS50181; FBOX; 1
                                                                                                      SM00016; OPR; 1.
                                                                                                                      SM00256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                               PR00320; GPROTEINBRPT.
 PS00678;
PS50082;
                           PS00108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                      FBOX;
                                                                                                                                 TYRKINASE.
                         PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_DOM; 1.
PROTEIN_KINASE_ST; 1.
 WD_REPEATS_2;
             WD_REPEATS_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.8%;
27.8%;
                                                                                                                                                                                                                           Ser_thr_kin_actsite
                                                                                                                                                                                                                                           OPR.
                                                                                                                                                                                                                                                      F-box.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence up
Last annotation
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Pred. No. 5e-24.
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               UNKNOWN_4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                  Reiner O., Shmueli O.;
"Characterization of the chicken homolog of LIS1.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF113946; AAF18938.1; -.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                  Q9PTR5 PRELIMINARY; PRT; 410 AA.
Q9PTR5; O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                   PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
PROSITE; PS50282; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Repeat; WD_repeat.
                                                                                 PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00320; WD40; 7.
        SEQUENCE
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Kinase; R
Transferase; WD repeat
SEQUENCE 942 AA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           519 SGRVFRLQFDEFQIVSSSHDDTILIW 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50294; WD_REPEATS_REGION; 1.
ATP-binding; Kinase; Repeat; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             914 HETIFSLQFNNQKLITGSLDKLVKIW 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 GNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQ-YDDQ-KIV 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISTFIPSETROKNYVWTVQFDQSKIISSGKTGIIRIWDIYNERDSRSIGG------H 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRVLEGHE----ELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEH 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLYVSGSSDNTIRLWDIECGAC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FNNGM---MVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFD------DKY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ILTGHTGSVLCLQY------DERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLR 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLGDVENKCITSSLDKTIQLWDAETGSCLSTLR---GHTGGIYCVKTDQVATHGNGYNHL 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSLKGHSGCIKSVDYQRQSGSDVSRVFTASADFTCKIFSLKTKKTLFTYTNHQEAVTCIN 745
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 410 AA; 46664 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 365.5; DB 5
Pred. No. 1.5e-21;
FC5848D06E0DCA20 CRC64;
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RESULT 15
Q9GL51
AC Q9GL51
D Q9GL51
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DT 01-MAR
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OS SUS SC
CC EUKAY
OC EUKAY
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Best Local Similarity 29.5%;
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Q9GL51;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-UN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-UN-2001 (TrEMBLRel. 17, Last annotation update)
PLATELET_ACTIVATING FACTOR ACETYLHYDROLASE IB-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00320; WD40; 7.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Hydrolase; Repeat; WD_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF31958; AAG33867.1; ... InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagasaka T., Boulday G., Coupel S., Coulon F., Tesson Heslan J.-M., Soulillou J.-P., Charreau B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning of porcine PAF-AH Ib-alpha cDNA and expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
240 VRPNQDGTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISWAPESSYSSISEATGS
                                         396 V--DFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR-------
                                                                                                                                                                                                                      280 IVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRVWDVNTG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 KTLRVWDF-----KNKRCMKTLNAHEHFVTSLDFHKTAPYVVTGSVDQTVKVWE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 V--DFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 ECIRTMHGHDHNVSSVAIMPNGDHIVSASRDKTIKMWEVQTGYCV---KTFTGHREWVRM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 MYSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHTGKLLASCSADMTIKLWDFQGF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 IVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRVWDVNTG 337
                                                                                                                                                                          MVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHSGKLLASCSADMTIKLWDFQGF 182
                                                                                  ECIRTMHGHDHNVSSVAIMPNGDHIVSAARDKTIKMWEVQTGYCV---KTFTGHREWVRM
                                                                                                                            EMINTLIHHCEAVIHLRF--NNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEF--QIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSGAYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETKKSGKPGPFLLSGSRDKTIKMWDISTGMCLMTLVGHDNWVRGVLFHSGGKFILSCADD
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                                                                                                                                                                                                                                                                                                                                                                                       410 AA;
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                                                                                                                                                                                                                                                                                                                                                                              46654 MW; A08DAFCD8B8B2719 CRC64;
                                                                                                                                                                                                                                                                                           11.6%; Score 351; DB 6; 28.9%; Pred. No. 7.7e-21;
                                                                                                                                                                                                                                                                 58; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 356; DB 13; Length 410; Pred. No. 3e-21;
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	Db	Qy	Db	Qy
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Search completed: May 8, 2002, 10:53:44
Job time: 226 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2002, 10:50:48; Search time 13.31 Seconds (without alignments) 1567.414 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-601-168A-2 3034 1 MDPAEAVLQEKALKEMNSSE......paaQAEPPRSPSRTYTYISR 569

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	21	Result
2384.5 1635.5 590.5 590.5 575 575 531.5 531.5 455.5 455.5 455.5 396.5 336.5 337 339.5 334.5 334.5 334.5 3324.5 3324.5 3324.5 3324.5 3324.5 3324.5 3324.5 3324.5 3324.5 3324.5 3324.5 324.5	3006 2597	Score
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273	276.5	277	280	280.5	281.5	283	283	283.5	285.5	287.5	290.5
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GBLP_MEDSA	YH92_CAEEL	TU12_SCHPO	GBLP_DROME	NUDF_EMENI	TUP1_KLULA	TUP1_YEAST	PRP5_SCHPO	GBLP_ARATH	T2D4_YEAST	GBLP_BRANA	TU11_SCHPO
024076 medicago sa			018640 drosophila			P16649 saccharomyc		024456 arabidopsis			Q09715 schizosacch

ALIGNMENTS

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AND DEGRADATION. F A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMATION: CYTOPLASMIC. DUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE ERNATIVE SPLICING. TAINS 1 F-BOX DOMAIN. TAINS 7 WD REPEATS (TRP-ASP DOMAINS).	"The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically with phosphorylated destruction motifs in I-kappa-B-alpha and beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro."; Genes Dev. 13:270-283(1999). -:- FUNCTION: BINDS SPECIFICALLY TO PHOSPHORYLATED IKB ALPHA (PIKAPPABALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR	Pagano M.; "Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179(1999). [4] CHARACTERIZATION. MEDLINE-99145464; PubMed-9990852; Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,	[3] SEQUENCE FROM N.A. (ISOFORM 2). MEDLINE-20003060; PubMed-10531035; Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,	SEQUENCE FROM N.A. (ISOFORM 2). TISSUS-Lymphoid; MEDLINE-98325370; PubMed-9660940; Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V., Thomas D., Strebel K., Benarous R.; "A novel human WD protein, h-beta TrCp, that interacts with HIV-1 Vpu connects CD4 to the ER degradation pathway through an F-box motif."; Mol. Cell 1:565-574(1998).	SEQUENCE FROM N.A. (ISOFORM 1). SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE=99075339; PubMed=9859996; Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M., Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.; "Identification of the receptor component of the IkappaBalpha- ubiquitin ligase."; Nature 396:590-594(1998).	_ 1	

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VARSPLIC
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SMART; SM0320; WD40; 7.
PROSITE; PS50181; FBOX; 1.
PROSITE: PS00678; WD_REPEATS_1; 6.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REPEAT
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VLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV
                VLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNISTCEFVRTLNGHKRGIACLQYRDRLVV
                                                                    SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFUNGMMVTCSKDRSIAVWDMASPTDITLRR
                                                                                                            ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                                     ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                                                                  GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
                                                                                                                                                                                 GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
                                                      SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR
                                                                                                                                                                                                                                            TTALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWR
                                                                                                                                                                                                                                                                                               PKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 144
                                                                                                                                                                                                                                                                                                                                                       NNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLANGTSSMIV 84
                                                                                                                                                                                                                                                                                                                                                                                                                         MDPAEAVLQEKALKFM-----NSSEREDC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    603482;
                                                                                                                                                                                                                          ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWR
                                                                                                                                                                                                                                                                                PKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF
                                                                                                                                                                                                                                                                                                                                        NNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLANGTSSMIV 120
                                                                                                                                                                                                                                                                                                                                                                                              MDPAEAVLQEKALKFMCSMPRSLWLGCSSLADSMPSLRCLYNPGTGALTAFQNSSEREDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00646; F-box;
PF00400; WD40; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF101784; AAD08702.1; -. Y14153; CAA74572.1; -.
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94.08;
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Pred. No. 1.1e-219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F-BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WD repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4C67F3B7E400FD37 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 605;
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Pfam; PF00646; F-box; Pfam; PF00400; WD40; 7 PRINTS; PR00320; GPROTI

SM00256; FBOX; 1. SM00320; WD40; 7.

GPROTEINBRPT.

InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.

U63922;

AAB49672.1; -.

M98268; AAA02810.1; -. U63921; AAB49671.1; -.

entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hudson J.W., Alarcon V.B., Elinson R.P.;

"Identification of new localized RNAs in the Xenopus oocyte by differential display PCR.";

Dev. Genet. 19:190-198(1996).

-i- FUNCTION: PROBABLY RECOGNIZE AND BINDS TO SOME PHOSPHARYLATED PROTEINS AND PROMOTES THEIR UBIQUITINATION AND DEGRADATION.

-i- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPIRE CONTINUE AND STATEMENT OF THE COMPIRED CONTINUE AND STATEMENT OF THE COMPIRED CONTINUE AND STATEMENT OF THE CONTINUE AND STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRCB_XENLA STANDARD; PRT; 518 AA. 1931854; P70037; P70038; P70038; P70038; P70038; P70038; P70038; P70038; P70038; P70038; P70048; P70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97109804; PubMed=8952061;
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Xenopodinae; Xenopus.
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SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TADPOLE EMBRYO.
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RESULT 3
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D7 20-AUG
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PROSITE;
                                                  Q9UKBI; Q9Y4C6; Q9P2S8; Q9P2S9;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
F-BOX/MD-REPEAT PROTEIN 1B (F-BOX AND WD-REPEATS
FBXW1B OR FBW1B OR BTRCP2 OR KIAA0696.
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                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                    FW1B_HUMAN
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                                                                                                                                                                       RVIITGSSDSTVRVMDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVMDMASP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens (Human)
                                                                                                                                                                                                                           YRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                                                                                                                                                                                                     TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
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                                                                                                                                                                                                                 YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
                                                                                                                                                                                                                                                           TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
                                                                                                                                                                                                                                                                                                                                             QRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLMGHTGSVLCLQYDE
                                                                                                                                                                                                                                                                                                                                                                                       RTDSLWRGLAERRGWGQYLFKNKPPDGKTPPNSFYRALYPKIIQDIETIESNWRCGRHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                 PMLQRDFITALPARGLDHIAENILSYLDAKSLCSAELVCKEWYRVTSDGMLWKKLTERMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50181;
PS00678;
PS50082;
PS50294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conjugation;
119 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  518
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230
270
310
353
393
433
482
302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FBOX; 1.
; WD_REPEATS_1; 6.
; WD_REPEATS_2; 7.
; WD_REPEATS_REGION; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258
298
338
381
421
461
510
304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59507
                      Primates;
                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.6%;
91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
WD 7.
GEM -> EFR (IN REF. 2).
GEA -> AAH (IN REF. 2).
GAA -> CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2597;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F-BOX.
                      Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                    542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
.2e-189;
                                                                                                                    A
                       Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TKLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                 Euteleostomi;
                                                                 BETA-TRCP2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                        515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                           402
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                                                                                                                                                                                                                                                                                                                                                                                        222
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REPEAT
REPEAT
VARSPLIC
VARSPLIC
                                                                                                                               Ubiquitin
DOMAIN
                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and
chromosome 5q35.1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=20003060;
                                                                     REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
-I- FUNCTION: PROBABLY RECOGNIZE AND BINDS TO SOME PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Katoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20160458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pagano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cenciarelli C., Chiaur D.S.,
                                                                                                                                                     PROSITE; PS00678; PROSITE; PS50082; PROSITE; PS50294;
                                                                                                                                                                                                                                                           EMBL; AB033281; BAA92331.1; EMBL; AB014596; BAA31671.1; ALT_INIT. InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98403880; PubMed=9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain
  SEQUENCE
                                                                                                                                                                                        PROSITE; PS50181;
                                                                                                                                                                                                                         PRINTS; PR00320; GPROTEINBRPT
                                                                                                                                                                                                                                    Pfam; PF00646; F-box; Pfam; PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Prediction of the coding sequences of unidentified human genes. X The complete sequences of 100 new_cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kotani H., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishikawa K.-I., Nagase T., Suyama M., Miyajima
                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROMOTES THEIR UBIQUITINATION AND DEGRADATION.
SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE
SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL),
ALTERNATIVE PRODUCTS: 3 ISOFORMS; A, B AND C (SHOWN HERE);
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                          AB033279;
AB033280;
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                                                                                                                                                                                                                                                                                                                                 AF176022;
                                                                                                                                                                                                  SM00256; FBOX;
SM00320; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sagara N., Kirikoshi
                                                                                                                              conjugati
129
  542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tion of a family of human F-box proteins."; 9:1177-1179(1999).
                                                                     238
238
278
318
361
401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tung;
  AA;
                                                                                                                                                                                                                                                                                                                      AAF04528.1; -.
BAA92329.1; -.
                                                                                                                                                                                                                                                                                                           BAA92330.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10531035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10694485;
                                                                                                                                                      WD_REPEATS_REGION;
                                                                                                                                                               WD_REPEATS_1; 5. WD_REPEATS_2; 7.
                                                                                                                                                                                        FBOX;
                       167;
167
275
315
315
398
440
478
478
494
494
494
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   62090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic structure of the betaTRCP2
                                                                                                                                           Repeat; WD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE
  ¥
F-BOX.

WD 1.

WD 2.

WD 3.

WD 4.

WD 5.

WD 6.

WD 7.

MISSING (IN ISOFORM A).

CSYPRSLWIGGANLVESMCALSCLOSMPSVRCL ->

MEDQNEDESPKRNTLW (IN ISOFORM B).

MEDQNEDSPKRNTLW (IN SOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guardavaccaro D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                н.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269:103-109(2000).
                                                                                                                                          repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takagi A., Miwa T., Hirai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of unidentified human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPLICING
                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B AND C (SHOWN HERE); ARE
                                                                                                                                            Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N., Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parks W.,
                                                                                                                                            splicing
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vidal
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                                                                                                                                                                                                                                                                                                                                                                                                                     collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                    outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEX
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                                                                                                                                                                                                                                                                                                                                                                                    commercia]
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Query Match

Local

Similarity

78.6%; 79.0%;

Score 2384.5; DB 1 Pred. No. 8.6e-173;

DB 1;

Length 542;

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YSS1_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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                                                                                                                                                                                                                                                                                                                                                Q0990;
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
HYPOTHETICAL 80.3 R
                                                                                                                  Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).-!- SIMILARITY: STRONG, TO X.LAEVIS BETA-TRCP.
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                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Rhabditidae; Pelodej
                                                                              between
                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                     CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            512
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                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                       CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WQRVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTILIWDFLNVPPSAQNETRSPSRTYTYISR 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLKVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S--TAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEP-DSVIEDKTIELMCS-------VP-----RSLWLGCANLV---ESMCAL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCLQSMPSVRCL---QISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                 Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                     36,
36,
                                                                                                                                                                                                                                                                            Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
TRP-ASP REPEATS CONTAINING PROTEIN K10B2.1 IN
                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                 Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4±;
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JOB

F-box.

F-box.

F-box.

F-box.

F-box.

F-box.

F-box.

F-box.

1.

JOB PROJEINBRPT.

JOB PROSITE; PS00320; GPROTEINBRPT.

JOB PROSITE; PS50181; FBOX; 1.

JOB PROSITE; PS50181; FBOX; 1.

PROSITE; PS50181; FBOX; 1.

DR PROSITE; PS50181; WD_REPEATS_2; 7.

DR PROSITE; PS50181; WD_REPEATS_2; 7.

DR PROSITE; PS50181; WD_REPEATS_2; 7.

DR PROSITE; PS50181; WD_REPEATS_1; WD repeat.

REPEAT 256 WD 1.

REPEAT 256 324 WD 2

REPEAT 379 407

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Best Local :
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InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
Pfam; PF00646; F-box; 1.
Pfam; PF00400; VD40; 7.
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 527
                                                                                                                            407
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                                                                                                                                                                                                                                                      287
                                                                                                                                                                                                                                                                                                                                  236 YPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKN 295
                                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 LKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIER 195
                                                                                                                                                                                                                                                                                                                                                                                                            196 MVRTDSLWRGLAERRGWGQYL---------FKNKPPDGNAPPNSFYRAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 SFLFPSRNTQIFLSYSRSFSSFSEVL----KWSEHEQLDFMDKIVHRLSHYQLGKVDNF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 RKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN-------GTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RRFREGKRALKQRGRARDGGSIQALTVCVST----IERCF--TAVSNPIFFLFSTFFSVF
                                                                                                                                                                                                      NNGMMYTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW 415
                                                                                                                                                                                                                                                   SHDDTILIWDFLNDPAAQAEPPRSPSRT
                                                                        IRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSS
                                                                                                                                         NTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRC
                                                                                                                                                                                                                                                                                  TLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRF 355
SHDDTILIWDFLDAP----PSGLPSST
                                                             IRFDEKRIVSGAYDGKIKVWDLQAALDPRALSSEICLCSLVQHTGRVFRLQFDDFQIVSS
                                                                                                                        SMDTLEFVRTLAGHRRGIACLQYRGRLVVSGSSDNTIRLWDIHSGVCLRVLEGHEELVRC
                                                                                                                                                                                       ANGIMVTCSKDRSIAVWDMVSPRDITIRRVLVGHRAAVNVVDFDDRYIVSASGDRTIKVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                            IRPMLQRDFISNLPA----HLVELILFNVNSDSLKSCEEVSTSWRCALARGQHWKKLIEK 166
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Pred. No. 4.7e-116;
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Best Local
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01-FEB-1996 (Rel. 33, C
20-AUG-2001 (Rel. 40, I
20-AUG-2001 (Rel. 40, I
HYPOTHETICAL 58.3 KDA T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rajandream M.A., Walsh S.V.,
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McDougall R.C., Rajandream M.A., Barrell B.G., Brown S., Murphy L., Jones L., McNeil A., Harris D.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPAC29E6.01 OR SPAC30.05
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                  SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL136538; CAB66464.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 240-506 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4896;
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DOMAIN
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51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation
 SLSKEGVVAVYNHVRSLLFTDFTEVFP----EEVSLRVFSYLDQLDLCKCKLMSKRWKRL
                        QMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRV 182
                                                                       ENCVAK----TKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLIS 122
                                                KNVVSKVSDLTSCSDFSTSSPVPCLNPLS--
                                                                                                                                                                                                                                                                                                                                                                     PF00400; WD40; 7
                                                                                                 163;
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                                                                                                            Similarity
                                                                                                                                                                                                                                                                   PS00678; WD_REPEATS_1; 3.
PS50082; WD_REPEATS_2; 6.
PS50294; WD_REPEATS_REGION; 1.
ical protein; Repeat; WD_repeat.
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                                                                                                                                                                                  al protein; Repeat; V 116 W 1256 W 1259 298 W 301 338 W 301 386 W 388 426 W 427. 464 W W
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Last annotation update)
TRP-ASP REPEATS CONTAINING PROTEIN C29E6.01
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                                                                                               104;
                                                                                                                                                           WW;
                                                                                              Score 690; DB
Pred. No. 8.3e.
4; Mismatches
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                                                                                                                                                                                                                                                           F-BOX.
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                                                                                                           8.3e-45;
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                                                -----HENNRIDLIRDLLA 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
F-BOX/WD-REPEAT PROTEIN POF1.
POF1 OR SPAC57A10.05.C.
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P87053;
15-JUL-1998
          InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
Pfam; PF00646; F-box; 1.
                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                    Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.; Submitted (APR-1997) to the EMBL/GenBank/DDJ databases.
-i- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                 EMBL; AB032410; BAA84528.1;
                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         STRAIN=97
                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                           fission yeast."
                                                                                                                                                                                                                                                                                                                                                                                                                           Katayama S., Kitamura K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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                                                               EMBL; Z94864; CAB08168.1;
                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                         Systematic genome-wide analysis of F-box protein-encoding genes
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                                                                                                                                                                                      9
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PF00400;

WD40;

F-box; 1. WD40; 7.

PRINTS; PR00320;

GPROTEINBRPT

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RESULT
SCOB_EI
 OX OCC
                                                                                                                                                                                            B
                                                                                                                                                                                                               QY
                                                                                                                                                                                                                                             Дb
                                                                                                                                                                                                                                                                  Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                    Q00659;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SULFUR METABOLITE REPRESSION CONTROL PROTEIN.
NCBI_TaxID=5072;
          Eurotiales; Trichocomaceae;
                        Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                   Emericella nidulans (Aspergillus nidulans)
                                                   SCONB OR MAPB1
                                                                                                                             SCOB_EMENI
                                                                                                                                          EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
SEQUENCE
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00678; WD_REPEATS_1; 2. PROSITE; PS50082; WD_REPEATS_2; 7. PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00256;
SMART; SM00320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS5018:
                                                                                                                                                                                        497 KVWEACE------CVHTLKNHSEPVTSVALGDCEVVSGSEDGKIYLWLFNNAP 543
                                                                                                                                                                                                               493 KVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 550
                                                                                                                                                                                                                                             437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat;
                                                                                                                                                                                                                                                                                             381
                                                                                                                                                                                                                                                                                                                                                 321
                                                                                                                                                                                                                                                                                                                                                                         315
                                                                                                                                                                                                                                                                                                                                                                                                                                                    212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 KPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 SSMIVPKQRKLSASYEKEKELCVKYFEQWSE---SDQVEFVEHLISOMCHYQHGHINSYL 136
                                                                                                                                                                                                                                         VQSLALADSRLFSCSLDGTIKQWDIEKKKCVHTLFGHIEGVWEIAADHLRLISGAHDGVV
                                                                                                                                                                                                                                                                                         SGGKRITLR----GHTGPVNSVRIIRDRGLVLSGSDDSTIKIWSLETNTCLHTFSAHIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                DYPTSSNEETISSVKPPSPNSDSKFFLPFKTRPWKEVYAERCR----VECNWRHGR----
                                                                                                                                                                                                                                                                IACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKI 492
                                                                                                                                                                                                                                                                                                                   ASPTDITLRRVLVGHRAAVNVVDF---DDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRG
                                                                                                                                                                                                                                                                                                                                             FDQCKLISGSMDKTIRIWNYRTSECISILHGHTDSVLCLTFDSTLLVSGSADCTVKLWHF
                                                                                                                                                                                                                                                                                                                                                                     YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM 374
                                                                                                                                                                                                                                                                                                                                                                                             ---CRQVVLSGHSDGVMCLQLVRNILASGSYDATIRLWNLATFQQVALLEGHSSGVTCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                     RIHCR----SETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INRK-----CEKCGWGLPLLERNTLYAAKASIQKRYERLTKRGVDQAHESSPVKKAKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSLVRLDFLSLLPV----EISFRILSFLDARSLCQAAQVSKHWKELADDDVIWHRMCEQH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSM----HNELSGLSEKSRQRVEAVWAAFSEASCSERKLALQGILNNCSSSLLSFASSTL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRTDSLWRGLAERRGWGQYLFKN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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350
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510
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FBOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FBOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KPPDGNAPPNSF-----YRALYPKIIQDIETIESNWRCGRHSLQ
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299
339
379
420
460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
          Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 590.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189;
                      Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00320; GPROTEINBRPT SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-!- SIMILARITY: BELONGS TO THE MET30/SCON-2 FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50181; FBOX; PROSITE; PS00678; WD_REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U21220; AAC15905.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REGULATORY PROTEIN THAT CONTROL SULFUR METABOLITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natorff
                                                 436
                                                                                                                                                                                                 294
                                                                                                                                                                                                                                                323
412 IKVWNTSTCEFVRTLNGH-
                                                                                                                                                                                                                                                                                                                                                                                                                                               209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 VEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  263
                                                                                                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 LQGIMAQCCFPQLSYISATVRDLIRIDFITALP----PEIAFKILCYLDTTSLCKASQVS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINS
                                                                                                                                                                                            KNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHL
                                                                                                                                                                                                                                                                                                                                          DKGVVGPRSPDASAESPPSGKRKLEDDEVAVVKRHCSSLGSDAGVDKDSDFFKTRYRPWK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNK------- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPRESSION.
                                           HFDASILASGSVDKTVKIWNFEDKSTFSLR----GHTDWVNAVRVDTSSRTVFSASDDCT
                                                                                            RFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV--VDFDDKYIVSASGDRT 411
                                                                                                                                              TETGEELRTLRGHESGIRCLQFDDTKLISGSMDRTIKVWNWRTGECISTYTGHRGGVIGL
                                                                                                                                                                                                                                                EVYKDRFKVGTNWKYGR-----CSIKTFKGHTNGVMCLQFEDNILATGSYDTTIKIWD
                                                                                                                                                                                                                                                                                            KIIQDIETIESNWRCGRHSLQRIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWD
                                                                                                                                                                                                                                                                                                                                                                                         RGWRALADDDVVWHRMCEQHIHRK-----CKKCGWGLPLLDRKRLRESKREIELRATTW 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
347
387
427
466
508
553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                675
76070 |
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415
455
496
543
535
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26.9%;
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F-BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 575; DB 1
Pred. No. 6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **********
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D840D452E37B4C53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 168; Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7654321
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-KRGIAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
435
                                                 491
                                                                                                                                              435
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                                                                                                                                                                                                                                                375
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RESULT 8
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-NJG-2001 (Rel. 40, Last annotation update)
                               SGD; S0001308; MET30.
InterPro; IPR001810; F-box.
InterPro; IPR001869; WD40.
Pfam; PF00646; F-box; 1.
Pfam; PF00400; WD40; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                               Rajandream M.A., Riles L., Rowley N., Skelton J., Smith Walsh S.V., Whitehead S.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.-i- FUNCTION: NEGATIVELY REGULATES SULFUR AMINO ACIDS BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Batandream K. P. 170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Surdin-Kerjan Y.;
"Met30p, a yeast transcriptional inhibitor that responds to S-
"met30p, a yeast transcriptional inhibitor that responds to S-
adenosylmethionine, is an essential protein with WD40 repeats.";
Mo1. Cell. Biol. 15:6526-6534(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P39014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96069360; PubMed-8524217;
Thomas D., Kuras L., Barbey R., Cherest H., Blaiseau P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MET30 OR YIL046W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MET30 PROTEIN
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 SMART; SM00256; FBOX; 1.
                                                                                                                          EMBL;
                                                                                                                                                                             or send
                                                                                                                                                                                             entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: SEEMS TO INTERACT WITH MET4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                  PRINTS;
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                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY
                                                                                                                                                                                                                                                                                                                           PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                  GENES EXPRESSION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMGLEPNAAYSQSSAFGTSFDNGRAAPPRYMYTSALDSTIRLWETTTGRCLRTFFGHLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VWALGADTLRIVSGAEDRMIKIWD-----
                                                                                                                      Z46861; CAA86905.1; -.
L26505; AAA96717.1; -.
                                                                                                                                                                              an email to license@isb-sib.ch).
                  PR00320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                  GPROTEINBRPT
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SCO2_ ID AC DT DT DT DT

SCO2_NEUCR STANDARD,
Q01277;
Q1277;
15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SULFUR CONTROLLER-2 (SCON2).

RESULT

NEUCR

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Best Local
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REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPEKNSLRQTYNSCARLCLN-QETVCLASTAMKTENCVAK-TKLANGTSSMIVPKQRKLS
                                                                                                                                                                                                                                                                                                                                    ---GWGQYLFKNK------PPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQ
                                                                                                                                                                                                                                                                                                                                                                                    GLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERR-
                                                                                                                                                                                                                                                                                                                                                                                                               NSNDKIRKL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPEYNFTKFCYRHNPDIQFSPTHTACYKQDLKRTQEINANIAKLPLQEQSDIHHIISKYS
                      RAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTI 541
                                                                                                                                                                                                       FDDRKLITGSLDKTIRVWNYITGECISTYRGHSDSVLSVDSYQKVIVSGSADKTVKVWHV
                                                                                                                                                                                                                            YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM
                                                                                                                                                                                                                                                         --HCRIQEFKGHMDGVLTLQFNYRLLFTGSYDSTIGIWDLFTGKLIRRLSGHSDGVKTLY
                                                                                                                                                                                                                                                                               RIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ
                                                                                                                                                                                                                                                                                                          PNCGWGLPLLHMKRARIQQNSTGSSSNADIQTQTTRPWKVIYRERFKVESNWRKG-----
                                                                                                                                                                                                                                                                                                                                                             --QELSIKILSYLDCQSICNATRYCRKWQKLADDDRVWYHMCEQHI------DRKC
                                                                      ----DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP
                                                                                                   \tt VQKIIPLTIKDVENLATDNTSDGSSPQDDPTMTDGADESDTPSNEQETVLDENIPYPTHL
                                                                                                                            KRGIACLQYRD--RLVVSGSS-----
                                                                                                                                                    ESRTCYTLR----GHTEWVNCVKLHPKSFSCFSCSDDTTIRMWDIRTNSCLKVFRGHVGQ
                                                                                                                                                                              ASPIDITLRRVLVGHRAAVNVVDFDDKYI--VSASGDRTIKVWNTSTCEFVRTLNGH---
                                                 LSCGLDNTIKLWDVKTGKCIRTQFGHVEGVWDIAADNFRIISGSHDGSIKVWDLQSG---
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---KCMHTF---NGR--RLQRETQHTQTQSLGDKV
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368
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28.9%;
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WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
WD 8 (POTENTIAL).
M -> I (IN REF. 1).
M -> S135D4BCA2E1EB97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 545; DB 1;
Pred. No. 1e-33;
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REPEAT
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PROSITE; PS00678; WD_REPEATS_1; 2.

PROSITE; PS50082; WD_REPEATS_2; 6.

PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes a protein with beta-transducin repeats.";
Proc. Natl. Acad. Sci. U.S.A. 92:3343-3347(1995).
-!- FUNCTION: NEGATIVELY REGULATES SULFUR STRUCTURAL GENE EXPRESSION.
-!- INDUCTION: EXPRESSED ONLY UNDER LOW-SULFUR COMDITIONS.
-!- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-!- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00646; F-box; Pfam; PF00400; WD40; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                 177 KEWYRVTSDGMLWKKLIERMYRTDSLWRGLAERRGWGQYLFKNKP------
                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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STRAIN=74-OR23-1A;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
269 VY----RDRWQVSYNWKNSRYKLSVL---KGHENGVTCLQLDDNILATGSYDTTIKIWNI 321
                           235 LYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGYYCLQYDDQKIVSGLRDNTIKIWDK
                                                                                                                            155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95241499; PubMed=7724564;
                                                                                                                                                                                                                                                               Local
                                                                                                                      QRWRTLADSDAVWVRMCEQHVNRK-----CTKCGWGLPLLERKKLRNYTRQRQLAKGGP
                                                           QGRVTELADSHDSQDRSVNQHGKRPAAEAEEEDPIKKRQCMAAAEASKAVTQPKTRSWKA
                                                                                                                                                                               LQGILSQLCFPQLSFVSREVNEALKIDFISALPV----ELAQKVLCYLDTVSLTKAAQVS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS.
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SM00320; WD40; 7.
                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; GPROTEINBRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sordariaceae; Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulat
                                                                                                                                                                                                                                                                                                                          72189 MW;
                                                                                                                                                                                                                                                            17.5%; Score 531.5; 25.0%; Pred. No. 1.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; WD repeat.
                                                                                                                                                                                                                                             76;
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                                                                                                                                                                                                                                             180;
                                                                                                                                                                                                                                             Indels 177;
                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                          650;
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      PROSITE; PS50181; FBOX; 1.

PROSITE; PS00678; WD_REPEATS_1; 5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION;
                                                                            PRINTS; PR00320; GPROTEINBRPT SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 7.
                                                                                                                      Pfam; PF00646; F-box; 1
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SEL-10 PROTEIN.
SEL-10 OR F55B12.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SE10_
                                                                                                                                                                                                       EMBL; Z79757; CAB02129.1; -.
                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                        InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                        WormPep; F55B12.3;
                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S.J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       609 KCDATYTGHCGPVTCVGLSDSLMASGSEDGTIRLHSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510 LCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDF 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 450 NTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498 MSHAQIERAGSPGSHSSSHNLLPSSLPSGDEDVRHLYGSAFVADESRPLPPRYFMTGGLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTLECKRILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLR 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STMRLWDSATGRCLRTLFGHLEGVWSLAGDTIRVISGANDGMVKTWE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVWNTSTCEFVRTLNGHKRGI------------ACLQYRDRLVVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDGHLLASGSSDKTVKIFDFNSKETYCLK----GHSDWVNSTHVDIKSRTVFSASDDTTI
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P53699;
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SEQUENCE
Shieh J.C., White A.M., Rosamond J.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
Submitted: Separation of the Separation of Initiation of DNA REPLICATION AND SEPARATION OF THE SPINDLE POLE: BODIES TO POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
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REPEAT
                                                                                                                                                                                    01-OCT-1996
20-AUG-2001
                                                                  STRAIN-SGY126;
                                                                              SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=5476;
                                                                                                                      Saccharomycetales; mitosporic
                                                                                                                                Eukaryota; Fungi; Ascomycota;
                                                                                                                                           Candida albicans (Yeast)
                                                                                                                                                                        CELL DIVISION CONTROL
                                                                                                                                                                                                              01-OCT-1996
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                                                                                                                                                                                                                                                                                                       EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD 522
                                                                                                                                                                                                                                                                                                                            AGTICLRTLVEHSGRVFRLQ-FDEFQIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                         TSIRVWDFTRPEGQECVALLQGHTSLTSGMQLRGNILVSCNADSHVRVWDI---
                                                                                                                                                                                                                                                                                                                                                                                  NTIRLWDI----ECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAP
                                                                                                                                                                                                                                                                                                                                                                                                             AVRCVQFDGTTVVSGGYDFTVKIWNAHTGRCIRTLTGHNNRVYSLLFESERSIVCSGSLD
                                                                                                                                                                                                                                                                                                                                                                                                                            AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WSTVDGSLLHTLQGHTSTVRCMAMAGSILVTGSRDTTLRVWDVESGRHLA---TLHGHHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIHDDVLYTGSDDNTLKVWCIDKGEVMYTLYGHTGGVWTSQISQCGRYIVSGSTDRTYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDLNVHRFLKLQKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PN-SFYRALYPKIIQDI------ETIESNWRCGRHSLQRIHCRSETSKGVYCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFTRLLQESNMTNIRQLRAIIEPHFQRDFLSCLPV----ELGMKILHNLTGYDLLKVAQV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESSYSNGSSSSYNADKLSSSRPLQHKLDLSASPSRNNDLNPRVEHLIALFKDLSSAEQMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                      (Rel. 34, Created)
(Rel. 34, Last sequence up
(Rel. 40, Last annotation
ON CONTROL PROTEIN 4.
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Pred. No. 6.9e-32;
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WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
                                                                                                                    Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exeuropean Bioinformatics Institute. There are no restrictions of the control of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        division;
                                                                                                                                                                                                                                                                                                                                                                                                                              VSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEANQNHLVFKLLQKTTRPTLSTFNNLINNSLKRDILSNVPF----EVTMKILSYLDYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SESDOVEFVEHLISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136;
AAADATLRIWDAKTGELRSKLKGHGAAITCFEHDGLRVVSGS-EKMLKLWNV
                                            GSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRA
                                                                                           GHLDRVYSTAIDFHSKTCFSGSMDSNINVWNFETGELKKVLVGHASLVGLLDLVDDVLVS
                                                                                                                                          GH--RAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVS
                                                                                                                                                                                        YIETFEGEFDNPYLIAVLSGHTQSVRSISGYGNIIISGSYDSTVRVWDLLDDGHCTHVLQ
                                                                                                                                                                                                                                                                                    HIFRGHTSTIRCLDIIHPAVIGKNQDGEDIVFPEYPLLITGSRDHNIHVWKLPVVDDSQD
                                                                                                                                                                                                                                                                                                                                  NTLIHH-----CEAVLHL----RFNNG------MMVTCSKDRSIAVWDM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REWSTLPEINSAQVLYKK----RKIIVNRWMDPKFKPHRISVSGHGNKVVTCLQHDDEKV
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SM00320; WD40; 7.
E; PS50181; FBOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKI
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76090 MW;
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25.4%;
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Pred. No. 1.4e
95; Mismatches
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506 PAGTICIRTLYEHSGRVFRLQFD-----EFQIVSSSHDDTIL-IWDFLNDPAAQ

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                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saupe S., Turcq B., Begueret J.;
"A gene responsible for vegetative incompatibility in the function podospora anserina encodes a protein with a GTP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update
VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.
                                                                                                                                                                                          REPEAT
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                                                                                                                                                                                                                              REPEAT
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PROSITE: PS50082; WD_REPEATS_2; 10.
                                                                                                                                                                                                                                                                                                                                   SMART; SM00320; WD40; 10
                                                                                                                                                                                                                                                                                                                                                                               EMBL; L28125; AAA85775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Lasiosphaeriaceae; Podospora.
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Podospora anserina.
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                                   581 EMPDDVSDDPESLEEIVKLCGSFLIIRERTVYFVHQSAKDFLLGTASDKASNKASQEAFE
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              82 MIVPK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED
                                                         EPPRKIIPEKNSLRQTYNSCAR-LCLNQETVCLASTAMK----TENCVAKTKLANGTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homologous domain.";
162:135-139(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                     164;
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PF00400; WD40; 10.
                                                                                               Similarity
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Pred. No. 1.0
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                                                                                 Wood V., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.; Submitted (MAR-1998) to the EMBL/GenBank/DBBJ databases.
-!- FUNCTION: INVOLVED IN MAINTENANCE OF PLOIDY THROUGH PROTEASOME DEPENDENT DEGRADATION OF CDK INHIBITOR RUM1 AND S-PHASE INITIAL CDC18. FUNCTIONS AS A RECCONSTI
                                                                                                                                                                                                                                                                                                                                                                                                Kominami K., Toda T.;
Kominami K., Toda T.;
"Fission yeast WD-repeat protein popl regulates genome ploidy through "Fission yeast WD-repeat protein popl regulates genome ploidy through "Fission yeast WD-repeat protein popl regulates genome ploidy through "Fission yeast WD-repeat protein popl regulates genome ploidy through "Fission years" with the protein popl regulates genome ploidy through "Fission years" with the protein popl regulates genome ploidy through "Fission years" with the protein popl regulates genome ploidy through "Fission years" with the protein popl regulates genome ploidy through "Fission years" with the protein popl regulates genome ploidy through "Fission years" with the protein popl regulates genome ploidy through "Fission years" with the protein popl regulates genome ploidy through "Fission years" with the protein popl regulates genome ploidy through "Fission years" with the protein popl regulates genome ploidy through "Fission" with the protein popl regulates genome ploidy through "Fission" with the protein popl regulates genome ploidy through "Fission" with the protein popl regulates genome ploidy through "Fission" with the protein ploid the ploid the protein ploid the ploid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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SUBUNIT: BINDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKTIKIWDTASGTCTQTLEGHGGWVQSVVFSPDGQRVASGSDDHTIKIWDAVSGTCTQTL
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                                                                SUBSEQUENTLY UBIQUITINATED AND TARGETED TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 36, Created)
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TO CDC18
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                                                                26S PROTEASOME
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00646; F-box; 1
Pfam; PF00400; WD40; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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InterPro; IPR001680; WD40.
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 553 NPDQNNDFTSATTNPFYIRTLRGHTDSVREVACL---GDLIVSASYDGTLRVWKASTGVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                          RHSLQRIHCRSETSKGVYC---LQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSV
                                                                                                                                                                                                                                                                                                                                                                                                                      TFSLDAPNNSVNYSYFSPNLLGNDSKTRQSFPPHSSSSSHNSLHEPVIYDFSSENPSIHP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEKALKFMNSSEREDC------NNGEPPRKIIPEKNSLRQTY-NSCARLCLNQET 56
                                                                                       VWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWN--------
                                                                                                                    WTFEYVGDTLVTGSTDRTVRVWDLRTGECKQVFYGHTSTIRCIKIVQGNQSTTDTD----
                                                                                                                                                                                                                                                                      ERMYRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCG
                                                                                                                                                                                                                                                                                                    LTGFPA----EITNLVLTHLDAPSLCAVSQVSHHWYKLVSSNEELWKSLFLKDGFFWDSI
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                                                                                                                                                                                                                                                                                                                                                            SNHLSSQKNAVLKLAQLISSFEKLPESVRQYLLFHLLSRCGKHAVQNIHKILLPIFQKNF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REKCLKRRNSSLSSNLHANKRFLFNSQSDGNKKNETFPSTNYSNVFYPNNCDSKEVASET
                                                                                                                                                  LCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIA
                                                                                                                                                                               LHAPEKIKRCSFPIHGVRLITKLQFDDDKIIVSTCSPRINIYDTKTGVLIRSLEEHEGDV
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                            TSTCEFVRTLNGHK----RGIACLQYRDRLVVSGSSDNTIRLWDIECGAC
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WD_REPEATS_2; 4.
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25.8%;
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Pred. No. 1.2e-26;
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                                                                                                                                                                                                                                          Length 775;
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P07834; P1788 (Rel. 08, Created)

01-NOV-1995 (Rel. 32, Last sequence up

20-AUG-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA
REPLICATION AND SEPARATION OF THE SPINDLE POLE BODIES TO FORM
POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD
DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND
VARIOUS ASPECTS OF SPORULATION. REQUIRED FOR HTA1-HTB1 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyan Yamazaki M., Tashiro H., Eki T.; Yamazaki M., Tashiro H., Eki T.; Sasanuma Yanalysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL DIVISION CONTROL PROTEIN 4. CDC4 OR YFL009W.
                                                                                   PIR;
SGD;
                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                InterPro; IPR001680; '
Pfam; PF00646; F-box;
Pfam; PF00400; WD40;
                                                                                                                  EMBL; X05625; CAA29113.1; -. EMBL; D50617; BAA09229.1; -. EMBL; D31600; BAA06495.1; -. EMBL; Z46255; CAA86341.1; -.
                                                                                                                                                                                                      entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S288C / AB972;
Barrell B.G., Churcher C., Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288C / AB972;
MEDLINE=95400292; PubMed=7670463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yochem J., Byers B.;
"Structural comparison of the yeast cell division cycle gene CDC4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88011240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-579 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Genet. 10:261-268(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661 LVSQVTFNQNILVSASAPPDTSLRVWD 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 LRVLEGHEELVRCIRFDNKR--IVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSG 520
                                                                   nterPro; IPR001810;
                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                        VARIOUS ASPECTS OF SPORULATION. REQUIRED TRANSCRIPTION ACTIVATION.
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                                                                                  A26867; A26867.
S0001885; CDC4.
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                                                 IPR001680; WD40.
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                                                                                                                                                                                                                                                         ormatics Institute. There are no restrictions on institutions as long as its content is in no
                                                                                                                                                                                                                      agreement (See http://www.isb-sib.ch/announce/
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PRINTS; PR00320; GPROTEINBRPT

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Best Local
 POP2
         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
WD-REPEAT_PROTEIN POP2_(PROTEOLYSIS FACTOR SUD1).
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50181, FBOX; 1.
PROSITE; PS500878; WD_REPEARS_1; 4.
PROSITE; PS50082; WD_REPEARS_2; 5.
PROSITE; PS50294; WD_REPEARS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                              649
                                                                                                                                                                       536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
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                                                                                                                                                                                                                                                                                                     469
                                                                                                                                                                                                                                                                                                                                                         452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 TYCLASTAMKTENCVAKTKLANGTSSMTVPKQRKLSASYEKEK-----ELCVKYFEQW 108
 OR
                                                                                                                                                                   SHDDTILIWDFLNDPAAQAEPPRSPSRTYTY 566
                                                                                                                                            AADGSIRGWD-AND-----YSRKFSY 668
                                                                             SCHPO
                                                                                                                                                                                             SMDTTIRIWDLENIWNNGECSYATNSASPCAKILGAMYTLQGHTALVGLLRLSDKFLVSA
                                                                                                                                                                                                                     AYDGKIKVWDL------VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS
                                                                                                                                                                                                                                                                                                                          VDFDD----KYIVSASGDRTIKVWNT------STCE----FVRTLNG
                                                                                                                                                                                                                                                                                                                                                                              TGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV
                                                                                                                                                                                                                                                                                                                                                                                                                       DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE-RVIITGSSDSTVRVWDVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSLNLKLSQKYPKLSQQDRLRLSFLENIFILKNWYNPKFVPQRTTLRGHWTSVITCLQFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTPLAKTTKTINN------NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK-- 244
                                                                                                                                                                                                                                                HMASVRTVSGHGNIVVSGSYDNTLIVWDVAQMKCLYILSGHTDRIYSTIYDHERKRCISA
                                                                                                                                                                                                                                                                       HKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSG
                                                                                                                                                                                                                                                                                                 LDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRG
                                                                                                                                                                                                                                                                                                                                                                                                      DNYVITGADDKMIRVYDSINKKFLLQLSGHDGGVWALKYAHGGILVSGSTDRTVRVWDIK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPNSFYRALYPKIIQD------IET--IESNWRCGRHSLQRIHCRSETSKGVYCLQYD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IINSLGVSQNWNKIIRKSTSLWKKLLISENFV---------SPKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLEKNKPPDGN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NLLFRLVANMDRSELSDLGTLIKDNLKRDLITSLPF----EISLKIFNYLQFED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00256;
SM00320;
 SUD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272
380
420
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568
630
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779
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OR SPAC4D7.03
                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitosis; Sporulation; 2 319 F-BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FBOX; 1. WD40; 6.
                                                                                                                                                                                                                                                                                                                                                     86089 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 399;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F-BOX.
                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> E (IN REF. 1)
0348F2F8FA78F3BC
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                                                                            703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196;
                                                                                                                                                                                                                                                                                                                                                     ------HVFKGHNSTVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS500678; WD_REPEATS_1; 3.
PROSITE; PS50082; WD_REPEATS_2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50181; FBOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: PUTATIVE COMPONENT OF E3 (PROTEIN-UBIQUITIN LIGASE)
COMPLEX; TARGETS CYCLIN-DEPENDENT KINASE-PHOSPHORYLATED CDC18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98318628; pubMed=9653157;
Jallepalli P.V., Tien D., Kelly T.J.;
"sudl+ targets cyclin-dependent kinase-phosphorylated Cdc18 and Ruml proteins for degradation and stops unwanted diploidization in fissio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-!- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=972; Wolf D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
     155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 95:8159-8164(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1997)
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                                                      60
                                                                                                        96
                                                                                                                                                  14 KFMNSSERED--CNNGEPPRKI-----IPEKNSLRQTYNSCARLCL----NQETVCL
                                                                                                                                                                                                                              Local Similarity
NSISSNSDNFPPSPKV--DTSNTVSPGSKPISEDLEDLNLQSIVQTFEDLPEGIQ-SYAF
                                                 ASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEK-EKELCVKYFEQWSESDQVEFVE 118
                                                                                                   KFNESIENVSYKCLDHSPPDSVPGDFSISLVPQRNFL-YSHSSLPPKIISIDRNNRIKLD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z98602; CAB11275.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF038867; AAB95480.1; -. AF064515; AAC39496.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR00320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS FOR DEGRADATION.
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                                                                                                                                                                                                                                                                                                                                 703 AA;
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                236
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545
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                                                                                                                                                                                                                              13.1%;
23.3%;
                                                                                                                                                                                                                                                                                                                              79605 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                 92;
                                                                                                                                                                                                                           Score 396.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                      ****
                                                                                                                                                                                                                                                                                                                              0336A0568C152396 CRC64;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                              1.9e-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions on 
ng as its content is in no
                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
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                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL outstation
                                                                                                                                                                                                    163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
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                                                                                                                                                                                                    Gaps
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B	Qy	ф	Qγ	Ъ	Qy	В	Qy	Дb	Qy	ф	γQ	망	Ωу	Db	Qy	В	Qy
629	519	578	459	518	401	473	341	421	297	361	260	313	230	268	178	212	119
SGYISSFVSDEHKII-SGNDGSVKLWD 654	SGRVFRLQFDEFQIVSSSHDDTILIWD 545	TGTCKYVLEGHDAFYTLLNVFQNRLISGSADSTIRIWDLNTGKPLMVLPSN 628	CGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEH 518	DILVSGSYDSSIRIWRVSTGECLYHLRGHSLRIYSVLYEPERNICISGSMDKSIRVWDLS 577	KYIVSASGDRTIKVWNTSTCEEVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIE 458	KLPKNTDPPYLPDNTNSIDRWE-KNPYFVHTLIGHTDSVRTISGYG 517	NTLIHHCEAVLHLRENNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDD 400	AKCTHIFRGHISIIRCLEILVPSRLIRHGVEIVEPDQPYIVSGSRDHTLRVW 472	LECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEML 340	KDRIITTSGSGTIQIHNAITGVLEARLEGHKEGVWAVKIHENTLVSGSIDKTVRVWNIEK 420	IHCRSETSK-GVYCLQYDDQKIVSGLRDNTIKIWDKNT 296	QISDDYFPEIFKRHFLNRKRWLFPSIPPSHLSFPIHVPNFMITSLLLH 360	SFYRALYPKIIQDIETIESNWRCGRHSLQR 250	TWNRILDVHTSYWKHMFSLEGFQINENDWKYANPNLNRPPFLHND 31;	EWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPN 229	FQLLRSCNRQSMRLLLNECEPLLKKDILSNLPFSIVQSILLNLDIHSFLSCRLVSP 26	HLISOMCHYOHGH-INSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCK 17

Search completed: May 8, 2002, 10:54:21 Job time: 213 sec

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Perfect score: Run on: OM protein - protein search, using sw model Database Total number of hits satisfying chosen parameters: Searched: Scoring table: PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* May 8, 2002, 10:49:08; Search time 19.54 Seconds (without alignments) 2218.184 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 219241 segs, 76174552 residues US-09-601-168A-2 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd MDPAEAVLQEKALKFMNSSE......PAAQAEPPRSPSRTYTYISR 569

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ۍ.	4	ω	2	_		Vesur	D
290.5	292	297	299.5	305	307.5	312	312.5	313.5	318	330	332.5	337	339.5	341	354	354	396.5	399	453	455.5	519.5	520	531.5	545	590.5	690	1635.5	2597		2025	
	9.6		9.9			0	•	10.3	10.5	10.9	11.0	11.1	11.2	11.2	11.7	11.7	13.1	13.2	14.9	15.0	17.1	17.1	7.		19.5	22.7	53.9	5	1	Match I	ap or
614	659	502	1194	704	1693	876	714	376	422	333	317	1146	777	515	410	409	703	779	775	1356	267	579	650	640	605	506	701	518	1019011		
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S583U6	S38108	T41148	T03818	S33263	S76086	T51507	S56893	T19266	A56640	G85034	T46032	A55532	T41075	S19487	S48052	S36113	T43557	S56245	T45136	T18521	S62507	T22703	T46660	S49932	T38932	T50211	T16607	B48088		3	
WD-40 repeat regui	hypothetical prote	a	apoptotic proteina	transcription init	_	WD40-repeat protei		hypothetical prote	CDC4 repeat unit-c	probable WD-repeat	WD-40 repeat regul	myosin-heavy-chain	hypothetical WD-re	hypothetical prote	platelet-activatin	LIS-1 protein - hu	F-box/WD-repeat pr	cell division cont	WD repeat protein			hypothetical prote	æ	MET30 protein - ye	probable sulfur me	WD-repeat protein	hypothetical prote	beta-transducin re		Description	

	411					
270 270 270	271.5 271.5 270	273 272.5	276.5 274	278.5 277	283 280	287.5 285.5
8.9		9.0	9.1 9.0	9.2 9.1	9.3	9.5 4.5
504 651	817 451	325 1008	501 2241	380 586	713 494	327 798
NNN	200	N N	NN	2 2	NN	NN
T50983 T50289	S51445 S65162	T09613	T27513 T16064	T40283 T38992	JN0133 T19550	\$48839 \$34023
nypothetical protein WD repeat protein	probable membrane hypothetical prote	probable GTP-bindi hypothetical prote	hypothetical prote	beta-transducin - WD-40 repeat regul	WD-40 repeat regul hypothetical prote	guanine nucleotide TATA box-binding p

ALIGNMENTS

RESULT B48088

beta-transducin repeat-containing protein - African clawed N;Alternate names: beta-Trcp C;Species: Xenopus laevis (African clawed frog)

frog

A;Cross-references: GB:M98268; NID:g295542; PIDN:AAA02810.1; PID:g295543 C;Superfamily: unassigned WD repeat proteins; WD repeat homology C;Keywords: duplication C;Keywords: duplication F;431-462/Domain: WD repeat homology <WD1> A;Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase A;Reference number: A48088; MUID:93330289
A;Accession: B48088 C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000 Ωy Вb 2 DЬ ρ B Qy DЬ Q Вb Qy Дb Qy A; Molecule type: mRNA A; Residues: 1-518 <SPE> A; Status: preliminary R;Spevak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J. Mol. Cell. Biol. 13, 4953-4966, 1993 C; Accession: B48088 Query Match
Best Local Similarity Matches 488; 378 343 318 223 258 163 198 43 GTSSMIVPKORKLSANYEKEKELCVKYFEOWSECDOVEFVEHLISRMCHYOHGHINTYLK 102 78 13 ASEREDCURDEPPRKIITEKUTLRQ------TKLAN 42 RTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSL 257 TDITLRRVLVGHRAAVNVVDEDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437 RVIITGSSDSTYRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASP 377 GTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLK 137 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 402 RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASA 342 Conservative 85.6%; 91.6%; Score 2597; DB 2; Pred. No. 1.6e-193; 7; Mismatches 8; Length 518; Indels 30; Gaps 1;

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527 SHDDTILIWDFLDAP----PSGLPSST 549

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A:Gene: CESD:K10B2.1
A:Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: The sequence of C. elegans cosmiu Al, Reference number: 218545
A;Accession: T16607
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein K10B2.1 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16607
R;Miller, N.
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A;Residues: 1-701 <MIL>
A;Cross-references: EMBL:U28730; NID:g860694; PID:g860695; PIDN:AAA68258.1; CESP:K10B2.
A;Experimental source: strain Bristol N2
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A, Description: The sequence of C. elegans cosmid K10B2
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Best Local
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                                                                                                                                                                                                                                                         356 NNGMAVTCSKDRSIAVWDMASPTDITLRRYLVGHRAAVNVVDEDDKYIVSASGDRTIKVW
                                                                                                                                                                                                                                                                                                                          287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 NVRSDSLWWGLSEKRQWDKFLNISRDMSVRRICEKFNYDVNIKRDKLDQLILMHVFYSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 IRPMLQRDFISNLPA----HLVELILFNVNSDSLKSCEEVSTSWRCALARGQHWKKLIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 LKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIER 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 VAALDPRAPAGTICLRTIVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                     NTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRC
                    SHDDTILIWDFLNDPAAQAEPPRSPSRT 563
                                                                                                                                                                                                                                                                                                                                          TLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRF
                                                          IRFDEKRIVSGAYDGKIKVWDLQAALDPRALSSEICLCSLVQHTGRVFRLQFDDFQIVSS
                                                                                                  IRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSS
                                                                                                                                          SMDTLEFVRTLAGHRRGIACLQYRGRLVVSGSSDNTIRLWDIHSGVCLRVLEGHEELVRC
                                                                                                                                                                                                                                 ANGIMYTCSKDRSIAVWDMYSPRDITIRRYLYGHRAAVNYVDFDDRYIVSASGDRTIKYW
                                                                                                                                                                                                                                                                                                                    DYSCSRILSGHTGSVLCLQYDNRVIISGSSDATVRVMDVETGECIKTLIHHCEAVLHLRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFLFPSRNTQIFLSYSRSFSSFSEVL-----KWSEHEQLDFMDKIVHRLSHYQLGKVDNF 110
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Pred. No. 8.6e-
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A; Introns: 43/1; 74/3
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A; Residues: 1-506 < MCD>
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A; Accession: T50211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 -ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VII 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 QYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS----- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 LEDPGIWKALYMOKGWFVNENVLNEFEAWRRTHKFPOPRFENFLKOONIIGPYGTMFLPO 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 QMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 SLSKEGVVAVYNHVRSLLFTDFTEVFP----EEVSLRVFSYLDQLDLCKCKLMSKRWKRL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 ENCVAK----TKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLIS 122
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                                VAALDPRAPAGTLCLRTLVEH-----SGRVFRLQFDEFQIVSSSHDDTILIWDF 546
                                                                                                                                      YRDRLYVSGSSDNTIRLMDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                                                                                                                                                     ACM-HVLRGHLASVNSVQYSSKTGLIVTASSDRTLRTWDITTGHCIRIHAHQRGIACAQ
                                                                                                         YNGKFIVSGSSDLTIRIFEASSGKLLRMLQGHEDLIRTVRFNDEKIVSGGYDGTVRIWN-
                                                                                                                                                                                                                                                                                ITLRRVLVGHRAAVNVVDFDDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437
                                                                                                                                                                                                                                                                                                                                                                                            TGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVW--DMASPTD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSDGMLWKKLI------ERMVRTDSLWRG-----LAERRGWG------ 213
                                                                                                                                                                                                                                                                                                                                       SGSSDSTITIWDWQNRRPLKVYFGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFIF-----DSNGRPLLNWSYLY----KEHAHLDSNWRHGRFLVSTFNNPSIRFPADQDF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 104; Mismatches 167;
---FNTGEQHCVLHNSRNSRVFGLQFDHRRIIACTHSSEILVWNF 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.7%; Score 690; DB 2; 30.4%; Pred. No. 1.1e-45;
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probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000 C;Accession: T38932

Churcher,

C.M.; Wood, V.;

Barrell, B.G.;

T38932

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MET30 protein - yeast (Saccharomyces cerevisiae)
N; Alternate names: protein Y1905.02; protein Y11046w
C; Species: Saccharomyces cerevisiae
C; Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text.
C; Accession: $49932; $43750
R; Odell, C.; Bowman, S.
submitted to the EMBL Data Library, December 1994
A; Reference number: $49931
A; Accession: $49932
A; Molecule type: DNA
A; Residues: 1-640 < ODE>
A; Residues: 1-640 < ODE>
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A;Map position: 1
C;Superfamily: unassigned WD repeat proteins; WD repeat
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A; Residues: 1-605 <BAD>
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A;Cross-references: GB:247047; EMBL:Z46861; NID:g603997; PID:g763300; MIPS:YIL046w R;Thomas, D.; Cherest, H.; Barbey, R.; Surdin-Kerjan, Y. submitted to the EMBL Data Library, December 1993 A;Reference number: S43750 A;Accession: S43750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVWEACE-----CVHTLKNHSEPVTSVALGDCEVVSGSEDGKIYLWLFNNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSLVRLDFLSLLPV----EISFRILSFLDARSLCQAAQVSKHWKELADDDVIWHRMCEQH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKI 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- CRQVVLSGHSDGVMCLQLVRNILASGSYDATIRLWNLATFQQVALLEGHSSGVTCLQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIHCR----SETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYPTSSNEETISSVKPPSPNSDSKFFLPFKTRPWKEVYAERCR----VECNWRHGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSM----HNELSGLSEKSRQRVEAVWAAFSEASCSERKLALQGILNNCSSSLLSFASSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQSLALADSRLFSCSLDGTIKQWDIEKKKCVHTLFGHIEGVWEIAADHLRLISGAHDGVV 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGGKRITLR----GHTGPVNSVRIIRDRGLVLSGSDDSTIKIWSLETNTCLHTESAHIGP 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASPTDITLRRVLVGHRAAVNVVDF--DDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDQCKLISGSMDKTIRIWNYRTSECISILHGHTDSVLCLTFDSTLLVSGSADCTVKLWHF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INRK-----CEKCGWGLPLLERNTLYAAKASIQKRYERLTKRGVDQAHESSPVKKAKLD
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Pred. No. 7.5e-38;
%6; Mismatches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cosmid c57A10
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A;Gene: SGD:MET30
A;Cross-references: SGD:S0001308; MIPS:YIL046w
A;Map position: 9L
C;Superfamily: unassigned WD repeat proteins;
F;298-329/Domain: WD repeat homology <WD1>
F;398-369/Domain: WD repeat homology <WD2>
F;374-409/Domain: WD repeat homology <WD3>
F;417-450/Domain: WD repeat homology <WD4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Restidues: 1-60,'I',62-640 <THO>
A;Cross-references: EMBL:L26505; NID:g432493; PID:g432494
C;Genetics:
T46660
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                                                                                                              RAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTI 541
                                                                                                                                                                                   ----DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP
                                                                                                                                                                                                                           VQKIIPLTIKDVENLATDNTSDGSSPQDDPTMTDGADESDTPSNEQETVLDENIPYPTHL
                                                                                                                                                                                                                                                               KRGIACLQYRD--RLVVSGSS-----
                                                                                                                                                                                                                                                                                                      ESRTCYTLR----GHTEWVNCVKLHPKSFSCFSCSDDTTIRMWDIRTNSCLKVFRGHVGQ
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                                                                                                                                                    LSCGLDNTIKLWDVKTGKCIRTQFGHVEGVWDIAADNFRIISGSHDGSIKVWDLQSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167;
                                                                           -KCMHTF--
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                                                                           -NGR--RLQRETQHTQTQSLGDKV 609
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Pred. No. 2.7e-34;
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R:Kumar, A.; Paietta, J.V.

Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995

Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995

A:Title: The sulfur controller-2 negative regulator:

A:Reference number: Z23121; MUID:95241499

A:Accession: T46660

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-650 <KUM>
                                                                                                                                                                                                                                                                                                                                              sulfur controller-2 protein [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_c
                                                                                                                                                                                                                                                                                                                  C; Accession: T46660
                                                                                                                                                                                                       regulatory
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#text_change

21-Jul-2000

gene

of

Neurospora

crassa

encode

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A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                   hypothetical protein F55B12.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A; Gene:
                                     A;Cross-references: EMBL:Z79757; PI;
A;Experimental source: clone F55B12
                                                                           A; Residues: 1-579 <WIL>
                                                                                                A; Molecule type: DNA
                                                                                                           A: Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                         A; Accession: T22703
                                                                                                                                                           A; Reference number: Z19602
                                                                                                                                                                          submitted to the EMBL Data Library,
                                                                                                                                                                                                      C;Accession: T22703 R;Sims, M.
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A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position:
3
19/1; 354/1
C;Function:
A;Description: negatively regulates sulfur structural gene expression
A;Note: scon-2+ expression is dependent on CYS3 function and the bindi
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
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Matches 144;
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CESP: F55B12.3
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                                                                                                                                                                                                                                                                                                                                                                                     KCDATYTGHCGPVTCVGLSDSLMASGSEDGTIRLHSF 645
                                                                                                                                                                                                                                                                                                                                                                                                                        LCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDF 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STMRLWDSATGRCLRTLFGHLEGVWSLAGDTIRVISGANDGMVKTWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt KLWDLDTRQVIRTYEGHVGHVQQVLILPPEYEPDEEVLNGASQDNQDAMSVSSGGSGSPS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVWNTSTCEFVRTLNGHKRGI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELYC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDGHLLASGSSDKTVKIFDFNSKETYCLK----GHSDWVNSTHVDIKSRTVFSASDDTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV--VDFDDKYIVSASGDRTI 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETEECIRTLYGHTAGIRALQFDDSKLISGSLDHTIKVWNWHTGECLSTFAAHTDSVISVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGYYCLQYDDQKIVSGLRDNTIKIWDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGRVTELADSHDSQDRSVNQHGKRPAAEAEEEDPIKKRQCMAAAEASKAVTQPKTRSWKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRWRTLADSDAVWVRMCEQHVNRK-----CTKCGWGLPLLERKKLRNYTRQRQLAKGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VY----RDRWQVSYNWKNSRYKLSVL---KGHENGVTCLQLDDNILATGSYDTTIKIWNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQGILSQLCFPQLSFVSREVNEALKIDFISALPV----ELAQKVLCYLDTVSLTKAAQVS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.5%; Score 531.5; DB 2 25.0%; Pred. No. 3.1e-33; tive 76; Mismatches 180
                                                    PIDN:CAB02129.1; GSPDB:GN00023; CESP:F55B12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID: 9806757; PIDN: AAA68968.1; PID: 9806758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ACLQYRDRLVVS-----
                                                                                                                                                                              September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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286 DNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VIITGSSDSTVRVWDVNTGEMLNTL

DRTYSYWDYNSRFILYKLYGHSGSYLCLDFCRRNLLYSGSSDSTIIIWDWQNRRPLKYY

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hypothetical trp-asp repeat-containing protein - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000 C;Accession: T38502; S62507 R;Jones, L.; Murphy, L.; McNeil, A.; Simpson, I.; Harris, D.; Barrell, B.G.; Rajandr
                                                                                                C;Superfamily: unassigned WD repeat proteins; F;18-51/Domain: WD repeat homology <WD1>F;104-137/Domain: WD repeat homology <WD2>
                                                                                                                                                             A; Map position: 1
                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                         A; Residues:
                                                                                                                                                                                                                                       A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                A; Reference number: Z21798
A; Accession: T38502
                                                                                                                                                                                                                                                                                                         Submitted to the EMBL Data Library, October 1995
A; Reference number 77777
                                                                                                                                                                                                                                                                                                                                                                                                                                                S62507
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A; Introns: 22/3; 45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3; 526/1
                        Query Match
Best Local
      Matches
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Best Local
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                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 QIHDDVLVTGSDDNTLKVWCIDKGEVMYTLVGHTGGVWTSQISQCGRYIVSGSTDRTVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 QYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 CDLNYHRFLKLQKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 PN-SFYRALYPKIIQDI------ETIESNWRCGRHSLQRIHCRSETSKGVYCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 CKEWYRVTSDGMLWKKL-IERMV-----RTDSLWRGLAERRGWGQYLFKNKPPDGNAP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 FVEHLISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 ESSYSNGSSSSYNADKLSSSRPLQHKLDLSASPSRNNDLNPRVEHLIALFKDLSSAEQMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 KTKLANGTSSMI------VPKQRK--LSASYEKEKEL------CVKYFEQWSESDQVE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
wes 150; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTLCLRTLVEHSGRVFRLQ-FDEFQIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTIRLWDI----ECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAP 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAIAAG-----VTIPDHIQP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFTRLLQESNMTNIRQLRAIIEPHFQRDFLSCLPV----ELGMKILHNLTGYDLLKVAQV 142
                                                                                                                                                                                                                     1-267 <JO2>
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                  EMBL: 266525;
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                      17.1%;
38.0%;
  58;
                                                                                                                                                                                                NID:g1044926;
                      Score 519.5; DB 2; Pred. No. 7.5e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 520; DB z; Pred. No. 2e-32;
    Mismatches
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                                                                                                                                                                                              PIDN:CAA91423.1; PID:g1044927; GSPDB:G
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  Indels
                                    Length
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Gaps
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C;Species: Podospora anserina
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18521
R;Saupe, S.; Turcq, B.; Begueret, J.
Gene 162, 135-139, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
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A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1356 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: A gene responsible for vegetative incompatibility in the fungus Podospora anser A;Reference number: Z18944; MUID:96009891 A;Accession: T18521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 IHHCEAVLHLRFNNGMMVTCSKDRSIAVW--DMASPTDITLRRVLVGHRAAVNVVDFDDK 401
     973
                                                                                                                                                                                                                                                                                        801
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                                                                                                913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    701 WIDHLRDLYSSTSSKWYHLLQDDGDIHRFLTTKYLYWLEALSLLRALP-EGINAIRQLES 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 641 LVFPTGIEDVSYIIFWRSLNVMSQKLRRDIYCLNAPGFLIDNVRVPDPDPLATVRYSCIY 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 MIVPK-----QRKLSASYEKEKE--LCVKYFEQWSESDQVEFVEHL--ISQMCHY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 EPPRKIIPEKNSLRQTYNSCAR-LCLNQETVCLASTAMK----TENCVAKTKLANGTSS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLMDIEC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SGRVFRLQFDEFQIVSSSHDDTILIWDF 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKLLRMLQGHEDLIRTVRFNDEKIVSGGYDGTVRIWN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEH- 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGLIVTASSDRTLRTWDITTGHCIRIIHAHQRGIACAQYNGKFIVSGSSDLTIRIFEASS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAEACM-HVLRGHLASVNSVQYSSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QHGHINSYLKP-----MLQRD-----FIT------ALPARGLDHI--AEN 159
     VAFSPDGQRVASGSGDKTIKIWDTASG---TCTQTLEGHGGSVWSVAFSPDGQRVASGSD
                                             LRFN-NGMMVTC-SKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDF--DDKYIVSASG
                                                                                                                                                                                                                                                                                                                                      FKNKPPDGNAPPNSFYRALY ----PKIIQDIETIESNWRCGRHSL-----
                                                                                                                                                                                                                                                                                                                                                                                      LLGHTIRGRLIA---IVRDGYRF---ALSYRMIIEKAPLQAYTSAL------V 800
                                                                                                                                                                                                                                                                                                                                                                                                                                      ILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIER --- MVRTDSLWRGLAERRGWGQYL 216
                                                                                                ASGTCTQTLEGHGGRVQSVAFSPDGQRVASGSDDHTIKIWDAASGTCTQTLEGHGSSVLS
                                                                                                                                           NTLECKRILTGHTGSVLCLQY--DERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLH 352
                                                                                                                                                                                                                                      -QRIHCRS-----ETSKG-------VYCLQY--DDQKIVSGLRDNTIKIWDK 294
                                                                                                                                                                                                                                                                                      F----APTDSMIKKIFKKEEPGWISTISVVEAEWNACTQTLEGHGSSVLSVAFSAD
                                                                                                                                                                                           GQRVASGSDDKTIKIWDTASGTGTQTLEGHGGSVWSVAFSPDRERVASGSDDKTIKIWDA 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL:L28125; NID:g607002; PID:g607003; PIDN:AAA85775.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.0%; Score 455.5; DB 2; 26.0%; Pred. No. 6.9e-27; ative 102; Mismatches 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 145; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FNTGEQHC 224
                                                     408
     1029
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C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Accession: T45135; T40157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: Fission yeast WD repeat protein Pop1
A; Reference number: Z22925
A; Accession: T45136
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A; Residues: 1-775 < WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z21842
A; Accession: T40157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: strain h- 972 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, submitted to the EMBL Data Library, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL:Y08391; PIDN:CAA69671.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-775 < KOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Kominami, K.; Toda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WD repeat protein popl [imported] - fission yeast (Schizosaccharomyces pombe
                                                                                                                              Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain 972h-; cosmid c2G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL022103; PIDN:CAA17898.1; GSPDB:GN00067; SPDB:SPBC2G2.18
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Best Local :
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390
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                                                                                                                                                                                                                                                                          241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 REKCLKRRNSSLSSNLHANKRFLFNSQSDGNKKNETFPSTNYSNVFYPNNCDSKEVASET 180
                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 QEKALKFMNSSEREDC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQF--DEFQIVSSSHDDTILIWDFLNDPAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKTIKIWDTASGTCTQTLEGHGGWVQSVVFSPDGQRVASGSDDHTIKIWDAVSGTCTQTL 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRTIKVWNTSTCEFVRTLNGHKRGIACLQYR--DRLVVSGSSDNTIRLWDIECGACLRVL 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGHEELVRCIRF--DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFR 524
LHAPEKIKRCSFPIHGVRLITKLQFDDDKIIVSTCSPRINIYDTKTGVLIRSLEEHEGDV 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGHGDSVWSVAFSPDGQRVASGSIDGTIKIWD----
                                           RHSLQRIHCRSETSKGVYC---LQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSV 310
                                                                                                                                  ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCG
                                                                                                                                                                                                                                                                          SNHLSSQKNAVLKLAQLISSFEKLPESVRQYLLFHLLSRCGKHAVQNIHKILLPIFQKNF 300
                                                                                                                                                                                                                                                                                                                                                                    TFSLDAPNNSVNYSYFSPNLLGNDSKTRQSFPPHSSSSSHNSLHEPVIYDFSSENPSIHP
                                                                                         DSKIRTMCLEQSLSA - -
                                                                                                                                                                                   LTGFPA----EITNLVLTHLDAPSLCAVSQVSHHWYKLVSSNEELWKSLFLKDGFFWDSI 356
                                                                                                                                                                                                                            ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYR-VTSDGMLWKKL------ 1 193
                                                                                                                                                                                                                                                                                                                      ----SYEKEKEL----CVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 144
                                                                                                                                                                                                                                                                                                                                                                                                                    VC-------LASTAMKTENCVAKTKLANGTSSMIVPKQRKLSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NNGEPPRKIIPEKNSLRQTY-NSCARLCLNQET 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 453; DB 2;
Pred. No. 4.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                            ----CAIMKRVYFRHFNLRERW---
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F;459-494/Domain:
F;628-659/Domain:
                                                                                                                                                                     A; Description: initiation of DNA replication; C; Superfamily: unassigned WD repeat proteins;
                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-779 < MUW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X05625; NID:g3502; PIDN:CAA29113.1; PID:g3503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-459, 'E', 461-779 <YOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z46255; NID:g559925; PIDN:CAA86341.1; PID:g559926; MIPS:YFL009:R;Yochem, J.; Byers, B.
J. Mol. Biol. 195, 233-245, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: $56245; $48310; A26867; $62304
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu submitted to the EMBL Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces ce A;Reference number: $56186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence_revision 12-Apr-1996 #text_change 26-May-2000
C;Accession: S56245; S48310; A26867; S62304
                                                                                                                                                       C; Keywords: cell cycle control
                                                                                                                                                                                                                         C; Function:
                                                                                                                                                                                                                                           A; Map position: 6L
                                                                                                                                                                                                                                                                                       A; Gene:
                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                            A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Murakami,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Structural comparison of the yeast cell division cycle gene CDC4 and a related A; Reference number: A26867; MUID:88011240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library,
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           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:D50617; NID:g836685; PIDN:BAA09229.1; PID:d1009870; PID:g83674
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A; Residues: 1-779 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell division control protein CDC4 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YFL009w
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                              Local
                                                                                                                                                                                                                                                                                       SGD:CDC4
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           139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPDQNNDFTSATTNPFYIRTLRGHTDSVREVACL---GDLIVSASYDGTLRVWKASTGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TSTCEFVRTLNGHK----RGIACLQYRDRLVVSGSSDNTIRLWDIECGAC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DVEKE-----NRPASNDANSMPPYIISSSRDCTIRLWSLPCLDDPPFVNVNE 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTFEYVGDTLVTGSTDRTVRVWDLRTGECKQVFYGHTSTIRCIKIVQGNQSTTDTD-----
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                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                          S62304
        Conservative
                                                                                                           WD repeat homology WD repeat homology
                                                                                                                                                                                                                                                               SGD:S0001885; MIPS:YFL009w
                                                                                                                                                                                                                                                                                                                 EMBL: D31600; NID: g836814; PIDN: BAA06495.1; PID: d1007066; PID: g83681
                                                                                                                                                                                                                                                                                                                                                                                                              S62302
                          13.2%;
                                                                                                                               homology <WD1>
        ;08
  Score 399; DB 2; Pred. No. 7.5e-23; 0; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  September 1994
                                                                                                                <WD2>
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                                                                                                                                                                         separation of the spindle pole bodies WD repeat homology
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                                              Length 779;
    Indels 156;
    Gaps
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    20;
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A;Reference number: Z22686; MUID:98318628
A;Accession: T43798
                                                                                                                                                 A; Residues:
                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                            A; Reference number: Z21812
A; Accession: T38794
                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-703 <WOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 AYDGKIKVWDL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                 1-703 <GEN>
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A;Cross-references: EMBL:Z98602; PIDN:CAB11275.1; GSPDB:GN00066; SPDB:SPAC4D7.03
A;Experimental source: strain 972h; cosmid c4D7
R;Jallepalli, P.V.; Tien, D.; Kelly, T.J.
Proc. Natl. Acad. Sci. U.S.A. 95, 8159-8164, 1998
A;Title: Sudl+ targets cyclin-dependent kinase-phosphorylated Cdc18 and Ruml proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F-box/WD-repeat protein pop2 - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: proteolysis factor sud1p
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Ju1-2000
C;Accession: T43557; T38794; T43798
R;Wolf, D.A.; Jackson, P.K.
submitted to the EMBL Data Library, December 1997
submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AF038867; PIDN:AAB95480.1
A;Experimental source: strain h- 972
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in A;Reference number: Z22576
A;Accession: T43557
                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; R submitted to the EMBL_Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        536 SHDDTILIWDFLNDPAAQAEPPRSPSRTYTY 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        589 SMDTTIRIWDLENIWNNGECSYATNSASPCAKILGAMYTLQGHTALVGLLRLSDKFLVSA 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 HKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 LDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 VDFDD----KYIVSASGDRTIKVWNT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 TGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE-RVIITGSSDSTVRVWDVN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 NSLNLKLSQKYPKLSQQDRLRLSFLENIFILKNWYNPKFVPQRTTLRGHMTSVITCLQFE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 APPNSFYRALYPKIIQD-----IET--IESNWRCGRHSLQRIHCRSETSKGVYCLQYD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 TTPLAKTTKTINN------NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IINSLGVSQNWNKIIRKSTSLWKKLLISENFV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK-----ELCVKYFEQW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --YSRKFSY 668
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IIS-1 protein - human
C;Species: Homo sapiens (man)
C;Date: 10-Dec.1993 #sequence_revision 10-Nov-1995 #text_change 26-May-2000
A; Status: preliminary A; Molecule type: mRNA
                                      A;Reference number: S36113; MUID:93361119
A;Accession: S36113
                                                                   R;Reiner, O.; Carrozzo, R.; Shen, Y.; Wehnert, M.; Faustinella, F.; Dobyns, W.B.; Caskey Nature 364, 717-721, 1993
A;Title: Isolation of a Miller-Dieker lissencephaly gene containing G protein beta-subun
                                                                                                                                                                                                                              RESULT 13
S36113
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                                                                                                                                            C; Accession: S36113
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C;Function:
A;Description: required to prevent spontaneous re-replication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 KFMNSSERED--CNNGEPPRKI-----IPEKNSLRQTYNSCARLCL----NQETVCL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pop2; sud1; SPAC4D7.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DILVSGSYDSSIRIWRVSTGECLYHLRGHSLRIYSVLYEPERNICISGSMDKSIRVWDLS 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRD--RLVVSGSSDNTIRLWDIE
                                                                                                                                                                                                                                                                                                                                                                                   TGTCKYVLEGHDAFVTLLNVFQNRLISGSADSTIRIWD----LNTGKP-----LMVLPSN
                                                                                                                                                                                                                                                                                                                                                                                                                         CGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEH 518
                                                                                                                                                                                                                                                                                                           SGYISSFVSDEHKII-SGNDGSVKLWD 654
                                                                                                                                                                                                                                                                                                                                               SGRVFRLQFDEFQIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWNRILDVHTS---YWKHMF-----SLFGFQINENDW-----KYANPNLNRPPFLHND 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQLLRSCNRQSMRLLLNECEPLLKKDILSNLPF----SIVQSILLNLDIHSFLSCRLVSP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLISOMCHYOHGH-INSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSISSNSDNFPPSPKV--DTSNTVSPGSKPISEDLEDLNLQSIVQTFEDLPEGIQ-SYAF 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKCTHIFRGHISIIRCLEILVPSRLIRHGVEIVEPDQPYIVSGSRDHTLRVW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LECKRILTGHTGSVLCLQY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFYRALYPKIIQDIETIESNWRCGRHSLQR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EWYRV----TSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPP----N 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KFNESIENVSYKCLDHSPPDSVPGDFSISLVPQRNFL-YSHSSLPPKIISIDRNNRIKLD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDRIITTSGSGTIQIHNAITGVLEARLEGHKEGVWAVKIHENTLVSGSIDKTVRVWNIEK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEK-EKELCVKYFEQWSESDQVEFVE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KLPKNTDPPYLPDNTNSIDRWE-KNPYFV---HTLIGHTDSVRTISGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.1%; Score 396.5; DB 2; Length 23.3%; Pred. No. 1e-22; tive 92; Mismatches 226; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -RHFLNRKRWLFPSIPPSHLSFPIHVPNFMTTSLLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g3293382; PIDN:AAC39496.1; PID:g3293383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----DERVIITGSSDSTVRVWDVNTGEML 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163;
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A;Accession: S51606
A;Accession: S51606
A;Accession: S51606
A;Molecule type: mRNA
A;Residues: 1-25, 'A',27-153, 'E',155-410 <HAW>
A;Cross-references: EMBL:D30615; NID:g516665; PIDN:BAA06305.1; PID:d1006869; PID:g551
C;Superfamily: unassigned WD repeat proteins; WD repeat homology <WD1>
F;104-137/Domain: WD repeat homology <WD2>
F;146-179/Domain: WD repeat homology <WD3>
F;188-221/Domain: WD repeat homology <WD3>
F;389-325/Domain: WD repeat homology <WD5>
F;380-265/Domain: WD repeat homology <WD5>
F;334-367/Domain: WD repeat homology <WD6>
F;376-409/Domain: WD repeat homology <WD6>
F;376-409/Domain: WD repeat homology <WD7>
                                                                                                                                                                                                                                                                                                             R;Hattori, M.
R;Hattori, M.
Submitted to the EMBL Data
Submitted to umber: S51606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:D30615
A;Note: the title has been revised in S48075
R;Hattori, M.; Adachi, H.; Tsujimoto, M.; Arai, H.;
Nature 370, 391-391, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Hattori, M.; Adachi, H.; Tsujimoto, M.; Arai, H.; Inoue, K.
Nature 370, 216-218, 1994
A;Title: Miller-Dieker lissencephaly gene encodes a subunit of brain platelet-activat A;Reference number: $48052; MUID:94301405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                platelet-activating factor acetylhydrolase 45K chain - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change C;Accession: S48052; S51606; S48075
                                                                                                                                                                                                                                                                                                                                                                                              A; Note: this is a revision to the title from reference
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S48075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Miller-Dieker lissencephaly gene encodes a subunit of brain platelet-activat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-410 <HAT>
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C:Superfamily: unassigned WD repeat proteins;
F:103-136/Domain: WD repeat homology <WDI>
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C; Genetics:
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F;375-408/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 IVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRVWDVNTG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 MVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHSGKLLASCSADMTIKLWDFQGF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECIRTMHGHDHNVSSVAIMPNGDHIVSASRDKTIKMWEVQTGYCV---KTFTGHREWVRM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRPNQDGTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISWAPESSYSSISEATGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87;
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                                                                                                                                                                                                                                                                                                                                            Library, April 1994
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homology <WD2>
homology <WD3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inoue, K.
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A; Residues: 1-484, 'I', 486, 'TKL', 490, 492-515 <BALL>
A; Cross-references: EMBL:X59720; MIPS:YCR072c
A; Note: this sequence has been revised in reference S26657
R; Ballesta, J.P.G.; Franco, L.; Hoenicka, J.; Jimenez, A.; submitted to the Protein Sequence Database, October 1992
A; Reference number: S26587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein YCR072c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 26-May-2000
C;Accession: S19487; S2657
R;Ballesta, J.P.G.; Franco, L.; Hoenicka, J.; Jimenez, A.; Remacha, M.; Sanz, E. submitted to the Protein Sequence Database, March 1992
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S19487
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A; Molecule type: DNA
A; Residues: 481-503 <BAL2>
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A; Accession: S19487
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490 GKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEF--QIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 ETKKSGKPGPFLLSGSRDKTIKMWDVSTGMCLMTLVGHDNWVRGVLFHSGGKFILSCADD 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 -----LVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSGAYD 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 V--DFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR------- 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 MVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHSGKLLASCSADMTIKLWDFQGF 182
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347 STPEEAQKKALENYEKICKKNGNSEEMMYTASDDYTMFLWNPLKSTKPIAR - - MTGHQKL 404
                                                                                                      287 GGQGLLYSGSHDRTVRVWDINSQGRCINILKSHAHWVNHLSLSTDYALRIGAFDHTGKKP 346
                                                                                                                                                          316 -DERVIITGSSDSTVRVWDVNT-GEMLNTLIHHCEAVLHLREN-----
                                                                                                                                                                                                                        236 SWEPIHLVKPGSK------PRLASSSKDGTIKIWDTVSRVCQYTMSGHTNSVSCVKW 286
                                                                                                                                                                                                                                                                               256 SLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQY 315
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                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRPNQDGTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISWAPESSYSSISEATGS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMINTLIHHCEAVLHLRF -- NNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                                                       89;
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30.8%;
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                                                       NG----MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAA 392
                                                                                                                                                                                                                                                                                                                                       Score 341; DB 2; Length 515; Pred. No. 1.3e-18; 7; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                          Indels 60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remacha,
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                                                                                                                                                                         ----- 356
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Search completed: May 8, 2002, 10:51:11 Job time: 123 sec

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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List...

A_Geneseq_1101:*
1: /SIDSB/gcgdata/
2: /SIDSB/gcgdata
3: /SIDSB/gcgdata
3: /SIDSB/gcgdat
4: /SIDSB/gcgda
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3034
     SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:

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SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:

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SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:

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SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDPAEAVLQEKALKFMNSSE......PAAQAEPPRSPSRTYTYISR 569
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1683.887 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		P				
Result		Query				
No.	Score	٦,	Length DB	B	ID	Description
1	3034	100.0	569	20	AAY24054	A human beta-trans
2	3034	100.0	569	21	AAB12813	Human beta-transdu
ω	3034	100.0	569	21	AAY96697	Human beta-TrCP.
4	3034	100.0	569	21	AAY83041	F-box protein FBP-
տ	3034	100.0	569	21	AAY83250	F-box protein hBet
6	3034	100.0	569	21	AAY44249	Human cell signall
7	3027	99.8	569	22	AAB48298	Human ZF11 protein
œ	3027	99.8	608	22	AAM00960	Human bone marrow
9	2997	98.8	569	21	AAB12812	Mouse ubiquitin li
10	2997	98.8	569	21	AAY83254	F-box protein FWD1
11	2962	97.6	590	22	AAM00847	Human bone marrow

F-box protein Pop2		2	703	13.1	396.5	5
F-box protein Cdc4		Ν	779	•	399	4
domain-c		느	779		399	ω
Amino acid sequenc		ņ	587		520	2
F-box protein Met3		N	640	18.0	545	Ξ
		2	669	•	640	0
		2	669	•	640	39
- 5	AAB5920	2	666	•	640	8
Human C-term mychi		2	666	21.1	640	7
Human hippocampal		2	627	•	640	36
Human hippocampal		2	627	21.1	640	35
Human hippocampal		2	592	•	640	34
Human hippocampal		2	592	•	640	ũ
Human mammary sel-		2	589	•	640	Ñ
Human GTPase assoc		N	589	•	640	÷
Human mammary sel-		2	589	21.1	640	Ö
	2 AAB59199	22	559	٠	640	ف
		2	559	•	640	8
		2	553	21.1	640	27
Human protein sequ		2	553	•	640	9
Human hippocampal		2	553	21.1	640	5
Human hippocampa		2	545	•	640	4
Human hippocampal		2(545	21.1	640	w
Human mammary se		2	540	•	640	Ñ
Human hippocampal		2	540	•	640	۳
Human mammary se	AAY2	20	540		640	0
Human hippocampal	AAY2246	20	540		4	φ
Protein encoded	AAB5920	22	626	•	44.	ω
Human 6myc-N-sel-	AAY2246	20	626	•		7
Beta-TRCP:N/SKP2	AAB4	N	448	•	ω	6
Human polypeptide	AAM4	22	550		384.	u
Human polypeptide	AAM4 02	22	542	•	384.	4
Human E3 ubiquitin	AAY966	21	542	78.6	2384.5	w
WD-40 domain-contg	AAR8585	16	517	•	582.	N

ALIGNMENTS

RESULT AAY24054

L

AAY24054 standard; Protein; 569 AA

30-SEP-1999 AAY24054;

(first entry)

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Beta-transducin repeat containing protein; beta-TrcP; Skplp; proteosome degradation pathway; Vpu protein; beta-catenin; proteosome deficiency virus-1; HIV-1; cellular protein; IKappaB; ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's; antiviral; antitumour; cell cycle regulation; protein degradation; and anti-inflammatory; osteo-articular inflammation; acute inflammation;
                                                                                                                                 Кеу
                                                                                                                                                                                                                                                            A human beta-transducin repeat containing protein.
Region
                  Region
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                                                                                                   Region
                                                                                                                       Region
                                                                                                                                                      Homo sapiens.
                                                                                                                                                                           tumour necrosis factor.
                                       Regior
                                                           Region
/note= "V
467..492
                   /note=
427..4
                                                             /note=
343..37
                                       /note= "WD motif" 387..415
                                                                                                                       Location/Qualifiers
                                                                                 304..332
                                                                                                    259..292
                                                                                                               note-
                                                             ..372
                    .455
          "WD motif"
                             "WD motif"
                                                                      "WD motif"
                                                                                        "WD motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      cc protein (beta-Trop). The protein directs proteins to the proteosome cc degradation pathways. The protein is able to interact with the Vpu protein of human immune deficiency virus-1 (HIV-1), cellular proteins cc IkappaB or beta-catenin (bC) and/or protein Skplp. The protein controls cc proteosomes for degradation. Depending on whether the process is cc inhibited or promoted, the result may be delayed breakdown of CD4 (in cc cases of HIV-1 infection); increased activity of IKB (and thus reduced cativity of NFkappaB) and increased degradation of mutant bC in tumour cc lls, or increased bC survival (and reduced apoptosis) in Alzheimer's cc patients. The beta-Trop protein, and its active peptide fragments, or its concleic acid, are used to screen for anti HIV-1 agents (antivirals), cantitumour agents that disrupt cells, and anti-inflammatory agents that disrupt activation by NFkappaB. Fragments of the protein are also useful for treating osteo-articular inflammaton or acute inflammation
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 569
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human beta-transducin repeat containing protein and its fragments useful as, or to screen for, antiviral, antitumour, anti-inflammatory and anti-Alzheimer's agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated with release of tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 60-61; 71pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX86501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-DEC-1998;
30-JAN-1998;
                              241 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRM ) INSERM INST NAT SANTE & RECH MEDICALE (INSP ) INST PASTEUR.
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241 qdietiesnwrcgrhslqrihcrsetskgvyclgyddqkivsglrdntikiwdkntleck
                                                                       181
                                                                                                                                            121
                                                                                                                                                                            121
                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                            1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence represents a human beta-transducin repeat containing
                                                                rvtsdgmlwkkliermvrtdslwrglaerrgwgqylfknkppdgnappnsfyralypkii
                                                                                  RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                                                                                     stamktencvaktklangtssm1vpkqrklsasyekekelcvkyfeqwsesdqvefvehl
                                                                                                                                                                                                                                                                            mdpaeavlqekalkfmnsseredcnngepprkiipeknslrqtynscarlclnqetvcla
                                                                                                                                                                     ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
                                                                                                                                                                                                                                           STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-469329/39.
                                                                                                                                                                                                                                                                                                                                                                  l Similarity
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                                                                                                                                                                                                                                                                                                                                                    Conservative
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98FR-0001100.
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                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 3034; 100.0%; Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "WD motif"
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                                                                                                                                                                                                                                                                                                                                                              3.2e-287;
                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
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                                                                                                                                                                                                                                                                                                                                                                              Length 569;
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                         The present invention describes an F-box motif protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin and is constituted by Skpl protein, Cull protein and a complex (SCF complex) of F-box protein containing F-box motif and WD40 repeat motif and has the amino acid sequence of 45 residues (AAB12811) or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1 protein) and (AAB12813, which is human beta-transducin repeat containing protein (beta-TrCP)). The F-box protein can be used fo the gene therapy of colon cancer by being recombined to a virus vector.
Sequence
                                                                                                                                                                                                        Claim 3; Page 10-12; 19pp; Japanese.
                                                                                                                                                                                                                                                        F-box protein of ubiquitin ligase SCF complex which promotes the
                                                                                                                                                                                                                                                                                              N-PSDB; AAA73132.
                                                                                                                                                                                                                                                                                                                WPI; 2000-485550/43.
                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP2000166542-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB; beta-catenin; Skpl; Cull; F-box motif; WD40 repeat motif; FWD1;
                                                                                                                                                                                                                                         ubiquitination of IkappaB or beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; colon cancer; beta-transducin repeat containing protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human beta-transducin repeat containing protein (beta-TrCP) SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB12813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB12813 standard; protein; 569
                                                                                                                                                                                                                                                                                                                                                (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
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Query Match
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Matches 569; Conserv

Conservative

100.0%; Score 3034; 100.0%; Pred. No. 3. 0

Mismatches

3.2e-287; DB 21;

Length 569;

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Gaps

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                     Manning A
Lavon I,
                                                                                                                                                                                                      anti-inflammatory;
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                                                                                                                                                                                                                                                                                                                 AAY96697 standard;
                                                                                                                                                         WO200034447-A2
                                                                                                                                                                               Homo sapiens
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  WPI; 2000-431294/37
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RES & DEV
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03-FEB-1999;
15-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and also major opportunistic infections, immune disorders, cardiovascular diseases and inflammatory disorders. FBP protein, analogs, derivatives and their subsequences, anti-FBP antibodies are also useful in diagnosis of the disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 their fragments are useful for screening compounds. The compounds are agonists or antagonists, which are useful for treating a proliferative or differentiative disorder in a mammal such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid for screening compounds useful for treating proliferative and differentiative disorders such as cancer and disorders comprises sequences encoding ubiquitin ligases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding substrate-targeting subunits of ubiquitin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligases with F-box motifs (F-box proteins) are useful for diagnosis of proliferative and differentiated related disorders by measuring
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181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
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                                                           ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 18C
                                                                                                                                                                                                                                       STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                                                                               mdpaeavlqekalkfmnsseredcnngepprkiipeknslrqtynscarlclnqetvcla 60
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99US-0124449.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 3034; DB 21; 100.0%; Pred. No. 3.2e-287;
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                                                                                                           Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with ubiquitin protein ligase or inhibiting ubiquitination using organic
                                                                                                                                                                                              Zhou P, Howley P;
                                                                                                                                                                                                                                            09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                             Ubiquitin ligase; SCF; F-box protein; targeted degradation; destabilisation; proteolysis; drug discovery; gene therapy;
                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                    (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                  08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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DB; AAZ93710.
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The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin ligases) which can be used for the targetted degradation of a target polypeptide in vivo. Targetted degradation is achieved by expressing the ubiquitin ligase in a cell linked to the interaction domain of the target polypeptide and thereby recruiting the target polypeptide to the ubiquitin ligase. Such methods are useful for decreasing or

Claim 9; Page 171; 185pp; English.

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RESULT
ARY44249
ID AXY4
XX AAY4
AC AAY4
XC AAY4
XX BEF
DT 28-F
XD EHUMB
XX Cell
KW infi
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Best Local S
Matches 569
Cell signalling protein-12; CSIGP-12; cell proliferation; inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS arteriosclerosis; Addison's disease; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mediated proteolysis. Degrading any desired protein in a cell is useful for preventing or treating diseases caused by the presence of abnormal amount of the specific polypeptides, for drug discovery and for gene therapy. Diseases treated include cancer, by degradation of oncoproteins, Huntington's disease, other proliferative disorders and microbial infections. The method provides a quick and easy alternative to gene knockout technology. The target polypeptide can be degraded at all stages, or a specific stage, of development in the
                                                                                            AAY44249;
                                                                                                                AAY44249 standard; Protein; 569
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                                                                                                                                                                                                                       KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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569; Conserv
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Pred. No. 3.2e-287;
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 Bandman O,
Baughn MR,
N-PSDB; AAZ29233
           WPI; 2000-086432/07
                                                                                      13-MAY-1998;
26-AUG-1998;
                                                                (INCY-) INCYTE PHARM INC
                                                                                                                        13-MAY-1999;
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Yang J;
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98US-0098010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is cell signalling protein-12 (CSIGP-12) encoded by cDNA obtained from Incyte clone 323149 of COLAUCTO1 library. It is expressed in musculoskeletal, gastrointestinal and nervous tissues and found to be homologous to beta-transducin repeats containing
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                                                                                                                                                     ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                          KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                                                                                                                                                      vtcskdrsiavwdmasptditlrrvlvghraavnvvdfddkyivsasgdrtikvwntstc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell signaling proteins useful for, ferative and inflammatory disorders
                                                                                                                     iliwdflndpaaqaepprspsrtytyisr 569
                                                                                                                                                                                      krivsgaydgkikvwdlvaaldprapagtlclrtlvehsgrvfrlqfdefqivssshddt
                                                                                                                                                                                                                                                                                           EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          569 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; l Bad; Bc1-2; tumour; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
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                                                                                                                                                                                                                                                                                QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK
                                                                                                                                                                    is {\tt qmchyqhghinsylkpmlqrdfitalpargldhiaenilsyldakslcaaelvckewy}
                                                                                                                                                                                                                           stamktencvaktklangtssmivpkqrklsasyekekelcvkyfeqwsesdqvefvehl 120
RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM
                                                     \verb|qdieties| nwrcgrhs| | qrihcrsets| kgvyclqyddqkivsglrdntikiwdkntleck| |
                                                                                                            {\tt rvtsdgmlwkkliermvrtdslwrglaerrgwgqylfknkppdgnappnsfyralypkii}
                                                                                                                            RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                                                                    ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELYCKEWY 180
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                                                                                                                                                                                                                                                                                                                                                          Similarity
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                             Mismatches
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1.6e-286;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUL-2000;
03-AUG-2000;
The present sequence is one of 251 novel human polypeptides encoded by a bone marrow-expressed polynucleotide. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
immunosuppressive; gene therapy; cytokine cell proliferation;
cell differentiation modulator; immune disorder; infection; c
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19-OCT-2000;
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JE, Wang J,
~ OA, Zhou J
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                                                                                                                                                                                                                                                                                                                                       treating e.g. cancer
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reating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                              10; Page 523-524; 648pp; English.
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ral; antibacterial; antifungal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boyle BJ,
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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2000US-0693036.
2000US-0250583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Asundi V, Chen R, u C, Xue AJ, Yang Y, Zha
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AAB12812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can used as nutritional sources or supplements and in the screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chemical compounds as potential drugs.
                                                                     Ubiquitin ligase SCF complex; F-box protein; ubiquitination; beta-catenin; Skpl; Cull; F-box motif; WD40 repeat motif; FWD gene therapy; colon cancer; beta-transducin repeat containing
                                                                                                                                                   27-NOV-2000
                                                                                                                                                                                                   AAB12812 standard;
                                   Mus musculus
                                                                                                                          Mouse ubiquitin ligase FWD1
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                                                                                                                                                                                                                                                                                                                              KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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                                                                                                                                                                                                                                                                 iliwdflndpaaqsepprspsrtytyisr
                                                                                                                                                                                                                                                                                                                  krivs gay dgkikvwdlvaaldprapagtlclrtlvehs grvfrlqfdefqivss shddt\\
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                                                                                                                                                   (first entry)
                                                                                                                                                                                                   protein;
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                                                                                                                        protein SEQ ID NO:2.
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No. 1.7e-286;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin and is constituted by Skpl protein, cull protein and a complex (SCF complex) of F-box protein containing F-box motif and wn40 repeat motif and has the amino acid sequence of 45 residues (AAB12811) or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWDl protein) and (AAB12813, which is human beta-transducin repeat containing protein (beta-TrCP)). The F-box protein can be used for the gene therapy of colon cancer by being recombined to a virus vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F\text{-}box protein of ubiquitin ligase SCF complex which promotes the ubiquitination of <code>IKappaB</code> or beta-catenin -
                                                                           481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                         241
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iliwdflndpaahaepprspsrtytyisr 569
                                  ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                {\tt krivsgaydgkikvwdlmaaldprapagtlclrtlvehsgrvfrlqfdefgivssshddt}
                                                                                KRIVSGAYDGKIKVWDLVAALDPRAPAGTICLRTILVEHSGRVFRLQFDEFQIVSSSHDDT 540
                                                                                                                                     efvrtlnghkrgiaclqyrdrlvvsgssdntirlwdiecgaclrvlegheelvrcirfdn
                                                                                                                                                                      EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 480
                                                                                                                                                                                                                            VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
                                                                                                                                                                                                                                                                             riltghtgsvlclqyderviitgssdstvrvwdvnagemlntlihhceavlhlrfnngmm
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                                                                                                                                                                                                         vtcskdrsiavwdmasptditlrrvlvghraavnvvdfddkyivsasgdrtikvwntstc
                                                                                                                                                                                                                                                                                                                                                   qdietiesnwrcgrhslqrihcrsetskgvyclqyddqkivsglrdntikiwdkstleck
                                                                                                                                                                                                                                                                                                                                                                                                                   rvtsdgmlwkkliermvrtdslwrglaerrgwgqylfknkppdenappnsfyralypkii
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98.6%;
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Pred. No. 1.3e-283;
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                                                                                                                   Matches
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                         the target polypeptide and thereby recruiting the target polypeptide to the ubiquitin ligase. Such methods are useful for decreasing or increasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF mediated proteolysis. Degrading any desired protein in a cell is useful for preventing or treating diseases caused by the presence of abnormal amount of the specific polypeptides, for drug discovery and for gene therapy. Diseases treated include cancer, by degradation of nncoproteins, Huntington's disease, other proliferative disorders and microbial infections. The method provides a quick and easy alternative to gene knockout technology. The target polypeptide can be degraded at all stages, or a specific stage, of development in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with using protein ligase or inhibiting ubiquitination using organic
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide in vivo. Targetted degradation is achieved by expressing the ubiquitin ligase in a cell linked to the interaction domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 184-185; 185pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ligases) which can be used for
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destabilisation; proteolysis; drug discovery; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oncoprotein; Huntington's disease; gene knockout; delivery systems;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F-box protein FWD1p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE.
                   61
                                                                                                                                   Local Similarity
                                             STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSBSDQVEFVEHL
                                                                                                                   561;
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                                                                                                                  Conservative
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                                                                                                                                98.8%;
98.6%;
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                                                                                                              Score 2997; DB 21;
Pred. No. 1.3e-283;
3; Mismatches 5;
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                                                                                                                                             Length 569;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; cell differentiation modulator; immune disorder; infection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bone marrow protein, SEQ ID NO:
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    WPI; 2001-488707/53
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2000US-0598042
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Best Local
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AAR85852 ID AAR8

AAR85852 standard; peptide;

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regions are involved in protein-protein interactions between proteins involved in intracellular signalling. An example of such an interaction is between protein kinase C and receptors of activated protein kinase (RACK), esp. RACK-1 (AAR85850). Proteins AAR85951-82 were isolated based on homology with beta-transducin, whereas proteins AAR85882-92 were isolated based on homology with the WD-40 consensus sequence (AAR8593). The proteins were used to construct the peptides AAR84928-R85063 and AAR85786-R85842. The peptides can be used to identify target proteins contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of proteins involved in protein-protein interaction and to screen for drugs that will affect the protein interaction and to screen for drugs that will affect the protein interaction and to screen for drugs that will affect the protein interaction and to screen for drugs that will affect the protein interaction and to screen for drugs that will affect the protein interaction and to screen for drugs that will affect the protein interaction and to screen for drugs that will affect the protein interaction and to screen for drugs that will affect the protein interaction and to screen for drugs that will affect the protein interaction and to screen for drugs that will affect the protein interaction and to screen for drugs that will affect the protein and to screen for drugs that will affect the protein and to screen for drugs that will affect the protein and to screen for drugs that will affect the protein and to screen for drugs that will affect the protein and to screen for drugs that will affect the protein and to screen for drugs that will affect the protein and to screen for drugs that will affect the protein and to screen for drugs that will affect the protein and to screen for drugs that will affect the protein and to screen for drugs that will affect the protein and the screen for drugs and the protein and the screen for drugs and the protein and the protein and the protein and the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the activity of a protein, eg. protein kinase C, which interacts with a protein contg. a WD-40 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins AAR85851-92 are protein which contain at least one WD-40 (also called beta-transducing homologous) amino acid repeat motifs. The WD-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WD40 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signalling; protein kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 80-82; 351pp; English.
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                                             QRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE 317
                                                                                                                                                                                                                                                                                                       rtdslwrglaerrgwgqylfknkppdgktppnsfyralypkiiqdietiesnwrcgrhsl
                                                                                                                                  RTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSL
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                                                                                                                                                                                                                                                             PMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMV
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Pred. No. 3.4
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                                                                                                                                                                                                     Polypeptide enhancing phosphorylated lkappaB ubiquitination useful treating disorder associated with NF-kappaB activation e.g. cancer comprising amino acid sequence of human E3 ubiquitin ligase or its
                                                                                                                                                                      Claim 1; Page 70-72; 77pp; English.
                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                            WPI; 2000-431294/37.
                                                                                                                                                                                                                                                                               Manning AM,
Lavon I, Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human E3 ubiquitin
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for use in treating diseases associated with activation of NF-kappa-B. I vitro analysis suggests that deletion of the F-box results in a protein that functions as a dominant negative molecule in vivo. Transient over-expression of delta-beta-TrCP (a deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha in stimulated Jurkat cells, resulting in accumulation of phosphorylated I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat inflammatory diseases,

autoimmune diseases,

cancer and viral infections

This is human E3 ubiquitin ligase (E3), which is homologous to human beta-TCCP, an F-box/MD protein family member. E3 enhances ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B degradation via the ubiquitin pathway is useful for identifying modulators of this process

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Best Local
                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
        26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                 Human polypeptide SEQ ID NO 3353.
                                                                                                                                                                                                                                                                                                 AAM40208 standard; Protein; 542 AA
                                                                                         Homo sapiens.
                                                                                                                                chemokinetic; thrombolytic; drug
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79.0%;
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Pred. No. 7.9e-224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                               screening; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide in gene therapy be used to treat diseases of the peripheral nervous contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.N.S disorders. Note: The sequence data for this patent did not form part of the printed \ensuremath{\mathsf{N}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assays for receptor activity, arthritis and inflammation,
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19-OCT-2000;
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                                                                                                                                                                 179 WYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPK
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                                                                                            212 iiqdietiesnwrcgrhnlqriqcrsenskgvyclqyddekiisglrdnsikiwdktsle
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MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDEDDKYIVSASGDRTIKVWNTS
                                                                                                           IIQDIETIESNWRCGRHSLQRIHCRSETSKGYYCLQYDDQKIVSGLRDNTIKIWDKNTLE
                                       clkvltghtgsvlclqydervivtgssdstvrvwdvntgevlntlihhneavlhlrfsng
                                                   CKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG
                                                                                                                                                  wqrvisegmlwkkliermvrtdplwkglserrgwdqylfknrptdg--ppnsfyrslypk
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Wang Z,
Zhou P,
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2000US-0598042.
2000US-0620312.
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2000US-0662191.
2000US-0693036.
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Wehrman T,
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79.0%;
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Pred. No. 7.9e
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Xu C, Xue
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nes 41;
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AJ,
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in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scierosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Parkhason's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating such as central nervous system injuries - \,
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25-APR-2000;
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                                                                                                                                                         Example 2; SEQ ID NO 6925; 10078pp; English.
                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
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                                                                                                  immunosuppressant
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                                                                                                  invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic, unosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD 538
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                                                                                                                                                                                                                                                                      Wang Z,
Zhou P,
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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Wehrman T,
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Xu C, Xue AJ,
R, Drmanac RT;
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Yang Y,
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Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                   WYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPK 238
                                                                                                                                                                                                                                                                                                                                                                                                               DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD
                                                                                                                                 TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 478
                                                                                                                                                                                                           MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTS 418
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                                                                                                                                                                                                                                                                                                                                                          wqrvisegmlwkkliermvrtdplwkglserrgwdqylfknrptdg--ppnsfyrslypk
                                                                                                                                                                                                                                                                                                                                                                                                                                             HLISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCKE 178
dtiliwdflnvppsagnetrspsrtytyisr
                            DTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                         \tt dnkrivsgaydgkikvwdlqaaldprapastlclrtlvehsgrvfrlqfdefqiissshd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451;
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79.0%;
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Pred. No. 8.16
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Search completed: May 8, 2002, 10:50:24 Job time: 111 sec

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Minimum DB
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  Score
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1: /cgn2_6/ptodata/2

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RESULT 1 US-08-190-802A-30 Sequence 30, Application US/08190802A Patent No. 5519003 Patent No. 5019003 Patent No. 5019003 Patent No. 5019003 Patent No. 5019003 Patent No. Dorit Patent No. Dorit Patent No. Dorit Patent No. Box 60850 Patent Patent No. Box 60850 COUNTER: CA PAPENT NO. Box 60850 COUNTER: CA PARTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 PAPENT APPLICATION DATA: PAPENT PAPENT PAPENT PAPENT NO BATA: PAPENT PAPENT PAPENT NO BATA: PAPENT PAPENT PAPENT PAPENT NO BATA: PAPENT PA	28 285.5 9.4 798 2 US-08-308-818-2 29 285.5 9.4 798 4 US-08-477-346-64 30 285.5 9.4 798 4 US-08-477-346-68 31 283.5 9.3 212 3 US-08-999-578-7 32 283 9.3 713 1 US-08-190-802A-63 33 283 9.3 713 1 US-08-190-802A-63 34 263 8.7 318 1 US-08-190-802A-63 35 263 8.7 318 4 US-08-477-346-63 36 260.5 8.6 375 4 US-09-063-743-1 37 256 8.4 996 1 US-09-063-743-1 38 256 8.4 996 1 US-08-190-802A-27 41 245.5 8.1 317 1 US-08-190-802A-47 42 245.5 8.1 317 1 US-08-190-802A-47 43 245.5 8.1 317 1 US-08-190-802A-47 44 245.5 8.1 317 1 US-08-190-802A-47 45 245.5 8.1 317 4 US-08-477-346-47 45 245.5 8.1 317 4 US-08-477-346-47 45 245.5 8.1 317 4 US-08-477-346-47
Uses	Sequence 2, Appli Sequence 64, Appl Sequence 68, Appli Sequence 63, Appli Sequence 63, Appli Sequence 33, Appli Sequence 31, Appli Sequence 31, Appli Sequence 5, Appli Sequence 27, Appli Sequence 27, Appli Sequence 41, Appl Sequence 47, Appl

Query Match Best Local Sim Matches 487;

Similarity

85.1%; 91.4%;

Score 2582.5; Pred. No. 5.5 Mismatches

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                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNBY/AGENT INFORMATION:
NAME: URDASCICE NAME:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                     REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
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APPLICANT: Ron, Dorit
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                                                                         NAME: MURASHIGE, KATE H. REGISTRATION NUMBER: 29,
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STATE: DC
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                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08899578 Patent No. 6087153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.1%;
Best Local Similarity 91.4%;
Matches 487; Conservation
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
ZIP: 10000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TYPE IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                              APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 /
                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE: BETA TRCP, Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                    462 VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 RIDSLWRGLAERRGWGQYLFKNKPPDGKTPPNSFYRALYPKIIQDIETIESNWRCGRHSL 222
                                                                    COUNTRY: UZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 RVIITG-SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 RTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 PMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMV 197
                                                                                                           STATE:
                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 PMLQRDFITALPARGLDHIAENILSYLDAKSLCSAELVCKEWYRVTSDGMLWKKLIERMY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 GTSSMIVPKORKLSANYEKEKELCVKYFEOWSECDQVEFVEHLISRMCHYOHGHINTYLK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 GTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 ASEREDCURDEPPRKITEKNTLRQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 SSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 517 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YRDRLYVSGSSDNTIRLWDIECGACLRYLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRIHCRSETSKGYYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLMGHTGSVLCLQYDE 282
                                                                                                                             New York
                                                                                                         New York
                                                                                                                                             E: Cooper & 1185 Avenue
                                                                                       U.S.A.
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                                                                                                                                                                                                                          SEL-10 AND USES THEREOF
                                                                                                                                             Dunham LLP
of the Americas
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Pred. No. 5.5e-266;
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                                                                                                                                                                                                                                                                                                                                                                                                                      514
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-899-578-2
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US-08-190-802A-32
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                                                                                                                                     Sequence 32, Application US/08190802A Patent No. 5519003
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
               GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 587 amino acids
TYPE: amino acid
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 SKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAIAAG-----VTIPDHIQP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 CKEWYRVTSDGMLWKKL-IERMV-----RTDSLWRGLAERRGWGQYLFKNKPPDGNAP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                              507 AGTLCLRTLVEHSGRVFRLQ-FDEFQIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                 440 TSIRVWDFTRPEGQECVALLQGHTSLTSGMQLRGNILVSCNADSHVRVWDI----
                                                                                                                                                                                                                                                                                                                                                                                                                              450 NTIRLWDI---ECGACLRVLEGHEELVRCIREDNKRIVSGAYDGKIKVWDLVAALDPRAP 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 QYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE~-RVIITGSSDSTVRV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 CDLNVHRFLKLQKFGDIFERAADKSRYLRADKIEKNWNANPINGSAV-LRGHEDHVITCM 262
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                                                                                                                                                                                                                                                                                    492 EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 AFTRILQESNMTNIRQLRAIIEPHFQRDFLSCLPV----ELGMKILHNLTGYDLLKVAQV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 ESSYSNGSSSSYNADKLSSSRPLOHKLDLSASPSRNNDLNPRVEHLIALFKDLSSAEOMD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 KTKLANGTSSMI------VPKQRK--LSASYEKEKEL-----CVKYFEQWSESDQVE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSTVDGSLLHTLQGHTSTVRCMAMAGSILVTGSRDTTLRVWDVESGRHLA---TLHGHHA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIHDDVLVTGSDDNTLKVWCIDKGEVMYTLVGHTGGVWTSQISQCGRYIVSGSTDRTVKV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : (212) 278-0400
(212) 278-0525
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Best Local Similarity 24.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 324-09 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown MOLECULE TYPE: protei HYPOTHETICAL: NO ANTI-SENSE: NO
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 779 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 IINSLGVSQNWNKIIRKSTSLWKKLLISENFV------SPKGF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 TTPLAKTTKTINN------NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK-- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. BOX
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                  277 DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE-RVIITGSSDSTVRVWDVN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                             452 KG----
                                                                                                                                                                                                                                                336 TGEMLNTLIHHCEAVLHLRFNNGMMYTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                392
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487 AYDGKIKVWDL-----
                                                                                                                         469 LDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRG
                                                                                                                                                                 396 VDFDD----KYIVSASGDRTIKVWNT-------STCE----FVRTLNG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 TYCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK------ELCVKYFEQW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: CDC4 / CDC20 protein, Fig. 15
                                                                                                                                                                                                                                                                                          DNYVITGADDKMIRVYDSINKKFLLQLSGHDGGVWALKYAHGGILVSGSTDRTVRVWDIK 451
                                                                                                                                                                                                                                                                                                                                                                              NSLNLKLSQKYPKLSQQDRLRLSFLENIFILKNWYNPKFVPQRTTLRGHMTSVITCLQFE 391
                                                                                                                                                                                                                                                                                                                                                                                                                     APPNSFYRALYPKIIQD-----IET--IESNWRCGRHSLQRIHCRSETSKGVYCLQYD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCAAELVCKEWYR-VTSDGMLWKKLI--ERMYRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NLLFRLVANMDRSELSDLGTLIKDNLKRDLITSLPF----EISLKIFNYLQFED 294
                                     HMASVRTVSGHGNIVVSGSYDNTLIVWDVAQMKCLYILSGHTDRIYSTIYDHERKRCISA 588
                                                                  HKRGIACLQYRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSG 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
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  ---VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80;
                                                                                                                                                                                                             Score 399; DB 1; Length 779;
Pred. No. 2.8e-33;
0; Mismatches 196; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 156; Gaps
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; ORIGINAL SOURCE: ; INDIVIDUAL ISOLATE: CDC4 / CDC20 protein, Fig. 15 US-08-477-346-32
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                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, App
Sequence 32, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2550-0025.20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: WD-40 - TITLE OF INVENTION: Thereof
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APPLICANT: Ron, Dorit
          295 IINSLGVSQNWNKIIRKSTSLWKKLLISENFV-----
                                           169 LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
                                                                                                                       109 SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                              194 TTPLAKTTKTINN------NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK-- 244
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                                                                                                                                                                                                      56 TVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK-----ELCVKYFEQW 108
                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                        139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acids
                                                                                   ---NLLFRLVANMDRSELSDLGTLIKDNLKRDLITSLPF----EISLKIFNYLQFED 294
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                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                 13.2%; Score 399; DB 4; Length 779; 24.3%; Pred. No. 2.8e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WD-40 - Derived Peptides and Uses
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                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                    196;
                                                                                                                                                                                                                                                Indels 156;
        --SPKGF 331
                                                                                                                                                                                                                                            Gaps
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                TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                              FILING DATE: 03-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                     REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1755 S. CITY: Arlington STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452 KG----
                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                             NAME:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & ADDRESSEE: NEUSTADT, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 TGEMLNTLIHHCEAVLHERFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
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    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMDTTTRIWDLENIWNNGECSYATNSASPCAKILGAMYTLQGHTALVGLLRLSDKFLVSA 648
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409 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
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IBM PC compatible
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В ρy В Qy 밁 Qy

amino acid

STRANDEDNESS: unknown

Gaps

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; ORGANISM: Bos taurus US-08-283-917-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08961716 Patent No. 5880272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME TITLE OF INVENTION: AND GENE THEREOF NUMBER OF SEQUENCES: 31
       REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 225
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                           ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5880272man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                               APPLICATION NUMBER: JP 209943/1993 FILING DATE: 03-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington
STATE: Virginia
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                                                                                                                                                                          APPLICATION NUMBER: US UFILING DATE: 03-AUG-1994
                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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ARAI, HIROYUKI
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TSUJIMOTO, MASAFUMI
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(703) 413-3000
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                                             2292-030-0
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
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ORIGINAL SOURCE:
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                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 KTLRVWDY------KNKRCMKTLNAHEHFVTSLDFHKTAPYVVTGSVDQTVKVWE 407
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STRANDEDNESS: unl
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                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                     STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington
                                                                                                CLASSIFICATION:
                                                                                                                APPLICATION NUMBER: FILING DATE: 03-AU
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Oblon,
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ARAI, HIROYUKI
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-200
TELEPAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                          PRIOR APPLICATION DATA:
                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME TITLE OF INVENTION: AND GENE THEREOF
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TOPOLOGY: ] in-
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                    APPLICATION NUMBER: US 0 FILING DATE: 03-AUG-1994
                                                                                 CLASSIFICATION:
                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                  CITY: Arlington
STATE: Virginia
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    APPLICATION NUMBER:
                                                                                                   FILING DATE:
                                                                                                                     APPLICATION NUMBER:
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INOUE, KEIZO
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                                      US 08/283,917
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JP 209943/1993
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5519003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51, Application US/08190802A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,875
                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: WD-40 - Derived Peptides and Uses TITLE OF INVENTION: Thereof
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ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5880272man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    490 GKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEF--QIVSSSHDDTILIWD 545
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                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 01-FEB-1994
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 11.7%; Score 354; DB 2; Length 410; Local Similarity 29.2%; Pred. No. 5.8e-29; les 87; Conservative 57; Mismatches 110; Indels
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                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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  8600-0139
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Best Local Similarity
         COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTI Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application US/08477346 Patent No. 6262023
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HYPOTHETICAL: N
ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER:
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29,959
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GENERAL INFORMATION:
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                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ron, Dorit TITLE OF INVENTION: WD-40 - TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
TELECOMMUNICATION INFORMATION:
                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 KTLRVWDY-----KNKRCMKTLNAHEHFVTSLDFHKTAPYVVTGSVDQTVKVWE 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             490 GKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEF--QIVSSSHDDTILIWD 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 V--DFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR------
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TYPE: amino acid
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                                      NAME: Fabian, Gary R. REGISTRATION NUMBER:
                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 01-FEB-1994
                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94306-0850
                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE: LIS1 (human), Fig. 34
                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                           STREET:
                       REFERENCE/DOCKET NUMBER:
                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMLNTLIHHCEAVLHLRF--NNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSGAYD 489
                                                                                                                                                                                                                                                                                                                                  CA
                                                                                                                                                                                                                                                                                                                                                                           P.O.
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                                                                                                                                                                                                                                                                                                                                                                         Box 60850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WD-40 - Derived Peptides and Uses
                                                                                                                                                US/08/190,802A
                                         33,875
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                       8600-0139
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 66
                APPLICATION NUMBER: 08/48
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H
REGISTRATION NUMBER: 29,5
                                                                                                                                                                        SOFTWARE: Patentin Rela
                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: WD-40 - Derived Peptides and Uses TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mochly-Ros
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 VNHVAFSPDGRYIVSASFDNSIKLWDGRDGKFISTFRGHIASVYQVAWSSDCRLLVSCSK 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 STPEEAQKKALENYEKICKKNGNSEEMMYTASDDYTMFLWNPLKSTKPIAR--MTGHQKL 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 -DERVIITGSSDSTYRVWDVNT-GEMLNTLIHHCEAVLHLRFN------ 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 DTTLKVWDVRTRKLSVDLPGIKTKLYVDWSVDGKRVCSGGKDKMVRLW 512
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REFERENCE/DOCKET NUMBER:
                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE: YCW2 PROTEIN, Fig. 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
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                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
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                                                                                                                                            07-JUN-1995
                                                                                                                                                                                                                  PC-DOS/MS-DOS
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                                                                                        08/487,072
                                                                                                                                                                                                                                                                                                                                                                                                               265
                                                                                                                                                             US/08/477,346
                  29,959
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2550-0025.20
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US-08-190-802A-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 52, Application US/08190802A Patent No. 5519003
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INFORMATION FOR SEQ
               NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Dei
TITLE OF INVENTION: Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 DTTLKVWDVRTRKLSVDLPGIKTKLYVDWSVDGKRVCSGGKDKMVRLW 512
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                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405 VNHVAFSPDGRYIVSASFDNSIKLWDGRDGKFISTFRGHIASVYQVAWSSDCRLLVSCSK 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 SWEPIHLVKPGSK------PRLASSSKDGTIKIWDTVSRVCQYTMSGHTNSVSCVKW 286
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                                                                                                                                                                                                                    COMPUTER:
                                                                                                                          FILING DATE:
                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dehlinger & Associates
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                                                                                                                                                                                                                                                                                                                                               P.O. Box 60850
                                                                                                                                                                                                                                                                                           USA
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SYSTEM: PC-DOS/MS-DOS
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(415)
                                                                                                           01-FEB-1994
N: 530
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                                                                                                                                           US/08/190,802A
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                                    8600-0139
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Pred. No. 2.4e-25;
                                                                                                                                                                                Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
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TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 1

52:

SEQUENCE CHARACTERISTICS:

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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MD6, Fig.
US-08-190-802A-52
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                 ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                 APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 YRDRLVVSGSSDNTIRLW----DIECGACLRVLEGHEELVRCIR----FDNKRIVS---- 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 AAVNVVDFDDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGI------ACLQ 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 KYFEQWSESDQVEF------VEHLISQMCHYQHGHINSYLKPMLQRDFITALPAR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watch 10.5%; Local Similarity 24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ---ELSFYLLKWLDPQTLLTCCLVSKQRNKVIS-----ACTEVWQTACKNLG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 422 amino acids TYPE: amino acid
                                                                                                                          COUNTRY:
                                                                                                                                                  STATE:
                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFD 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W-----QIDDSVQDSLHWKKVYLKAILRMKQLED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPGDYILLSADKYEIKIWPIGREINC-KCLKTLSVSEDRSICLQPRLHFDGKYIVCSSAL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAVESVDYSDELDILVSGSADFAVKVWALSAGTCLNTLTGHTEWVTKVVLQKCKVKSLLH 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WDVSTGQCVYGIQTHTCAAV---KFDEQKLVTGSFDNTVACWEWSSGARTQHFR---GHT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WDVNTGEMLNTL-IHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHR 390
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                                                                                                                                                                 Washington
                                                                                                                                                  g
                                                                                                                                                                                  2000 Pennsylvania Avenue,
                                                                                                                          USA
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  PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 318; DB 1; Length 422; Pred. No. 4.1e-25;
Version #1.25
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INFORMATION FOR SEO ID NO: 52
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
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APPLICATION NUMBER: US,
FILING DATE: 07-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
346 GLYQWDFASYDILRVIKTPEVANLALL-----GFGDVFALLFD 383
                                                 486 GAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFD 528
                                                                                                                                                                                                                                                                                                  173 WDVSTGQCVYGIQTHTCAAV---KFDEQKLVTGSFDNTVACWEWSSGARTQHFR---GHT
                                                                                                                                                                                                                                                                                                                                              332 WDVNTGEMLNTL-IHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHR 390
                                                                                                                                                                                                                                                                                                                                                                                               144 -----LIGHSARVYALYYKDGLLCTGSDDLSAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 WGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 KYFEQWSESDQVEF------VEHLISQMCHYQHGHINSYLKPMLQRDFITALPAR 151
                                                                                                                                                                                                                                           391 AAVNVVDFDDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGI------ACLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                           272 CLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 W-----QIDDSVQDSLHWKKVYLKAILRMKQLED-------HEAFETSS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 GLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ---ELSFYLLKWLDPQTLLTCCLVSKQRNKVIS-------ACTEVWQTACKNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KDFETWLDNISVTFLSLMDLQKNETLDHLISLSGAVQLRHLSNNLETLLKRDFLKLLPL- 62
                                                                                                                                                 YRDRLVVSGSSDNTIRLW----DIECGACLRVLEGHEELVRCIR----FDNKRIVS----
                                                                                                                                                                                             GAVFSVDYSDELDILVSGSADFAVKVWALSAGTCLNTLTGHTEWVTKVVLQKCKVKSLLH
                                                                                               SPGDYILLSADKYEIKIWPIGREINC-KCLKTLSVSEDRSICLQPRLHFDGKYIVCSSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5%; Score 318; DB 4; Length 422; 24.4%; Pred. No. 4.1e-25; tive 69; Mismatches 161; Indels 120;
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